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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 10:01:29 ; Search time 195 Seconds
(without alignments)
12987.389 Million cell updates/sec

Title: US-10-035-045-20
Perfect score: 3563
Sequence: 1 agcctggcagtgccctcagg.....tggacacccctgtgaccatc 3563

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	3.2	4134	3	US-09-162-021B-1
2	112.4	3.2	4134	4	US-09-687-477-17
3	112.4	3.2	4134	4	US-09-687-476-17
4	112.4	3.2	4134	4	US-09-687-372-17
5	112.4	3.2	4134	4	US-09-975-553-17
6	112.4	3.2	4134	4	US-10-270-795-17
7	112.4	3.2	4134	4	US-10-270-876-17
8	112.4	3.2	4134	4	US-10-268-051-7
9	111	3.1	2925	4	US-09-695-481-3
10	111	3.1	3234	4	US-09-016-434-1432
11	111	3.1	3809	1	US-08-485-588-3
12	111	3.1	3809	1	US-08-484-565-3
13	111	3.1	3809	2	US-08-480-751-3
14	111	3.1	3809	2	US-08-943-986-3
15	111	3.1	3809	2	US-08-353-784-3
16	111	3.1	3809	3	US-08-484-719B-3
17	111	3.1	3809	3	US-08-546-998-2
18	111	3.1	3809	3	US-08-484-159-3
19	111	3.1	4000	2	US-08-687-289A-2
20	111	3.1	4000	4	US-09-435-897-2
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22	111	3.1	5006	1	US-08-484-565-2
23	111	3.1	5006	2	US-08-480-751-2
24	111	3.1	5006	2	US-08-943-986-2
25	111	3.1	5006	3	US-08-353-784-2
26	111	3.1	5006	3	US-08-484-719B-2
27	111	3.1	5006	3	US-08-546-998-1

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29	109.2	3.1	2993	3	US-09-361-631-3	Sequence 3, Appli
30	109	3.1	2010	3	US-09-361-631-8	Sequence 8, Appli
31	108.8	3.1	2532	3	US-09-361-631-4	Sequence 4, Appli
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34	104.8	2.9	5275	2	US-08-480-751-1	Sequence 1, Appli
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38	104.8	2.9	5275	3	US-08-484-159-1	Sequence 1, Appli
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41	98.6	2.8	3177	3	US-09-134-513-1	Sequence 1, Appli
42	90.4	2.5	2148	5	PCT-US93-01642-1	Sequence 1, Appli
43	82.6	2.3	4131	1	US-08-485-588-4	Sequence 4, Appli
44	82.6	2.3	4131	1	US-08-484-565-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; CURRENT FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439) ... (3522)
US-09-162-021B-1

Query Match 3.2%; Score 112.4; DB 3; Length 4134; Best Local Similarity 46.3%; Pred. No. 2.9e-13; Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;					
QY	2422	GACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGAGCGAAGCACACGC	2481		
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QY	2482	TGCTTCGCGCAGGTCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGCTGTGCTGCTC	2541		
Db	2254	TGCATCGCCAAGGAGATCGAGTACCTTCGTGGACGAGCCCTTCGGGATCGCTCTGACC	2313		
QY	2542	CTGCTGTGAGCCTGGCGCTGGSCCTTGTGCTGGCTGCTTTGGGGCTGTTCTGTTACCAT	2601		
Db	2314	ATCTTCGCCCTACTGGGCATCCTGATCACCTCCTTCGTGCTGGGGTCTTCATCAAGTTC	2373		
QY	2602	CGGGACAGCCACTGTTTACGGCCCTCGGGGGGGCCCCCTGGCCCTGCTTGGCCTGGTGTGC	2661		
Db	2374	AGGAACACTCCCATCGTGAAGGCCAACACCGGGAGTTGTCTTACCTGCTGCTCTCTCC	2433		
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Db 2434 CTCATCTGCTGCTTCTCCAGCTCGCTCATCTTTCATCGCGAGCCAGGACTGGACCTGT 2493
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QY 2782 CAGGCGCCGAGATCTCGTGGAGTCAGAACTGCTCTGAGCTGGGAGAGCCGGCTGAGT 2841
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QY 2842 GGCTGCTGCGGGGCGCTGGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTG 2901
Db 2611 AAGTGGTGGGCTCAACCTGAGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2670
QY 2902 GCACTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2961
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QY 2962 CTGCCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3021
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QY 3022 CAGGCCACCAATGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3081
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QY 3202 CAGATGGGCGCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3261
Db 2971 GAGGTGATTGCCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3030
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RESULT 2

US-09-687-477-17
; Sequence 17, Application US/09687477
; Patent No. 6463883
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/09/687,477
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-477-17

Query Match 3.2%; Score 112.4; DB 4; Length 4134;
Best Local Similarity 46.3%; Pred. No. 2.9e-13;
Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;
QY 2422 GACGACATCGCCTGACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAGCACACGC 2481
Db 2194 GATGCAAGTGGTGTACAAAGTGGCGAATGATTCTTGTGCGAATGAGAACACACGTCG 2253

QY 2482 TGCTTCCGCGCAGGCTCTCGGTTTCTGCGATGCGGCGAGCCGCTGTGCTGCTGCTGCTC 2541
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QY 2542 CTGCTGCTGAGCCCTGCGCTGGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2601
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QY 2602 CCGGACAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2661
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QY 2662 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2721
Db 2434 CTCATCTGCTGCTTCTCCAGCTGCTCATCTTTCATCGCGAGCCCGAGGACTGGACCTGT 2493
QY 2722 CTGGCCAGCAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2781
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Db 2671 GTCACCTGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2730
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RESULT 3

US-09-687-476-17
; Sequence 17, Application US/09687476
; Patent No. 6475792
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; FILE REFERENCE: 2213.2001-000
; CURRENT APPLICATION NUMBER: US/09/687,476
; CURRENT FILING DATE: 2000-10-22


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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-476-17

Query Match      3.2%; Score 112.4; DB 4; Length 4134;
Best Local Similarity 46.3%; Pred. No. 2.9e-13;
Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;

QY 2422 GACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACACGC 2481
Db 2194 GATGCAAGTGCCTGTACAAAGTGCCCCGAATGATTTCTGGTGAATGAGAACACACGTCG 2253

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Db 2374 AGGAACACTCCCATCGTGAAGGCCACCAACCGGAGTGTGCTACCTACCTGCTCTCTCC 2433

QY 2662 CTGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2721
Db 2434 CTGATCTGCTGCTTCTCCAGCTCGCTCATCTTCTATCGCGGAGCCAGGACTGGACCTGT 2493

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QY 2902 GCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2961
Db 2671 GTCACCTGCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2730

QY 2962 CTGCCCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3021
Db 2731 GAGGACGAGTCTATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2790

QY 3022 CAGCCCAACCAATGCAACGCTGGCCCTTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTG 3081
Db 2791 ATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2850

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Db 2911 GTCTGGATCTCTTCTATCCCCGCTATGTACGACACCTACGGCAAGTTTGTGTCGGCCGT 2970

QY 3202 CAGATGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3261
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US-09-687-372-17
; Sequence 17, Application US/09687372
; Patent No. 6481379
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/09/687,372
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-372-17
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Query Match      3.2%; Score 112.4; DB 4; Length 4134;
Best Local Similarity 46.3%; Pred. No. 2.9e-13;
Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;

QY 2422 GACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACACGC 2481
Db 2194 GATGCAAGTGCCTGTACAAAGTGCCCCGAATGATTTCTGGTGAATGAGAACACACGTCG 2253

QY 2482 TGCTTCCGCCGAGGTCTCGGTTCTTGGCATGGGGCGAGCCGGCTGTGCTGCTGCTC 2541
Db 2254 TGCATGCCAAGGAGATCGAGTACCTGTCTGCGAGCGGCCCTTCGGGATCGCTCTGACC 2313

QY 2542 CTGCTGCTGAGCCTGGCGCTGGGCCCTTGTGCTGGCTGCTTGGGGCTGTTTCGTTACCAT 2601
Db 2314 ATCTTCGCCGTACTGGGCATCTCTGATCACCTCTTCTGCTGGGGTCTTTCATCAAGTTC 2373

QY 2602 CGGACAGCCCCACTGGTTTCAAGCCTCGGGGGGCCCTTGGCCCTGCTTGGCCCTGCTGTC 2661
Db 2374 AGGAACACTCCCATCGTGAAGGCCACCAACCGGAGTGTGCTACCTACCTGCTGCTTCTCC 2433

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QY 2782 CAGCGCGCGAGATCTTCTGAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2841
Db 2554 AAGACCAACCGGGTGTGCTGCTTCTCGA---GGCCAAGATCCCAACAGCCTCCACCGC 2610

QY 2842 GGCTGCCTGGGGGGCCCTGGGCCCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2901
Db 2611 AAGTGGTGGGCTCAACCTGCAGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2670

QY 2902 GCACCTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2961
Db 2671 GTACCTGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2730

QY 2962 CTGCCCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3021
Db 2731 GAGGACGAGTCTATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2790

QY 3022 CAGCCCAACCAATGCAACGCTGGCCCTTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTG 3081
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Db 2911 GTCTGGATCTCTTCTATCCCCGCTATGTACGACACCTACGGCAAGTTTGTGTCGGCCGT 2970

QY 3202 CAGATGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3261
Db 2971 GAGGTGATTGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3030

QY 3262 TGTACCTGCTCATGCGGAGCCAGGCTCAACACCCCCGAG 3303
Db 3031 TGTATCATCATCTGTTCAAGCCGTGCCGTAAACCATCGAG 3072
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Db 2374 AGGAACACTCCCATCGTGAAGGCCAACCAACGGGAGTTGTCTACCTGCTGCTCTCTCC 2433
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RESULT 7
US-10-270-876-17
; Sequence 17, Application US/10270876
; Patent No. 6655318
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134

; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17
Query Match 3.2%; Score 112.4; DB 4; Length 4134;
Best Local Similarity 46.3%; Pred. No. 2.9e-13;
Matches 408; Conservative 0; Mismatches 471; Indels 3; Gaps 1;
QY 2422 GACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCCGGAGGAAAGCACACGC 2481
Db 2194 GATGCAAGTGGTGTACAAAGTCCCCGAATGATTCTTGGTCGAATGAGAAACACACACGTCG 2253
QY 2482 TGCTTCGCGCGCAGGTCCTGGTTCCTGGCATGGGCGAGCCGGCTGTGCTGCTGTGCTC 2541
Db 2254 TGCATCGCCAAAGGAGATCGAGTACCTGTGCGTGGAGAGCCCTTCGGGATCGCTCTGACC 2313
QY 2542 CTGCTGCTGAGCCTGGCGCTGGGCTTGTGCTGGCTGCTTTGGGGCTGTTTGGTTCACCAT 2601
Db 2314 ATCTTCGCGTACTGGGCATCCTGATCACCTCCTTCGTGCTGGGGTCTTTCATCAAGTTC 2373
QY 2602 CGGGACAGCCCACTGGTTCAGGCCCTCGGGGGGGCCCCCTGGCCTGCTTGGCCCTGGTGTGC 2661
Db 2374 AGGAACACTCCCATCGTGAAGGCCAACCAACCGGGAGTTGTCTACCTGCTGCTCTTCTCC 2433
QY 2662 CTGGGCTGCTGCTGCTCAGCGTCTCCTCTGTTCCCTGGCCAGCCCCAGCCCTGCCCCGATGC 2721
Db 2434 CTCATCTGCTGCTTCTCCAGCTCGCTCATCTTCATCGGGAGCCCCAGGACTGGACCTGT 2493
QY 2722 CTGGCCCCAGCAGCCCTTGTCCCCACCTCCCGCTCACGGGCTGCCTGAGCACACTCTTCCTG 2781
Db 2494 CGGCTCCGCCAACCGGCTTGGCATCAGCTTCGTCTGTGTCATCTCCTGTCATCCTGGTG 2553
QY 2782 CAGGCGCGCGAGATCTTCGTGAGTCAAGACTGCTGCTGAGCTGGGAGACCGGCTGAGT 2841
Db 2554 AAGACCAACCGGCTGCTGGTCTTCGA---GGCCAAAGATCCCCACAGCCTCCACCGC 2610
QY 2842 GGCTGCTCGGGGGGCCCTGGCCTGGTGGTGTGCTGGCCATGCTGGCCTACTTCATC 2901
Db 2611 AAGTGGTGGGCTCAACCTGCAGTTCCTCTGCTCTCTCTGTCATCCTGGTGCAATC 2670
QY 2902 GCACTGTGCACCTGGTACCTGGTGGCCTTCCCGCCGAGGTGGTGAACGACTGGACATG 2961
Db 2671 GTCACCTGCATCATCTGGCTCTACACCGCGCCTCCTCCAGCTACAGGAACCATGAGCTG 2730
QY 2962 CTGCCCCAGGAGGCTGGTGCATGCTCCCGCACACGCTCCTGGGTGAGCTTCGGCCTAGCG 3021
Db 2731 GAGGACGAGGTCACTTCATCACCTGCAGCGAGGGCTCGCTCATGGCGCTGGGCTTCCTC 2790
QY 3022 CAGGCCACCAATGCCAGCTGGCCTTCTCTGCTTCTGGGCACTTTTCTGGTGGGAGC 3081
Db 2791 ATCGGCTACACCTGCTCCTCGCCGCTATGCTTCTTCGCTTCAAGTCCCGTAAG 2850
QY 3082 CAGCGGGCTGCTACAAACGCTGCGGCTCACCTTGGCCATGCTGGCCTACTTCATC 3141
Db 2851 CTGCGGAGAACTTCAAGGAGCTAAGTTTCATCACCTTCAGCATGTTGATCTTCTTCATC 2910
QY 3142 ACCTGGGTCTCCTTTGTGCCCCCTCCTGGCCAAATGTGAGGTGGTCTCAGGCCCGCGTG 3201
Db 2911 GTCTGGATCTCCTTTCATCCCGCCTATGTGAGCACCTACGGCAAGTTTGTGTGGCGTG 2970
QY 3202 CAGATGGGCGCCTCCTGCTGTGCTGCTGGGCATCCTGGCTGCCTTCACCTGCCCCAGG 3261
Db 2971 GAGGTGATTGCCATCTCGCCTCCAGCTTCGGGCTGTGGGCTGCATTTACTTCAACAAG 3030
QY 3262 TGTACCTGCTCATGCGGAGCCAGGGCTCAACACCCCGAG 3303
Db 3031 TGTATACATCCTGTTCAGCGCGTGGCGTAACACCATCGAG 3072

RESULT 8
US-10-268-051-7
; Sequence 7, Application US/10268051
; Patent No. 6748900

QY 1298 TTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCTGG 1357
 Db 838 ATCAAGGAGATTGTCCGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGCGAGGCTGG 897
 QY 1358 CTGACCTCTGACCTGGTCTATGGGCTGCCCGGCAATGCGCCAGATGGGCACGGTGTGGC 1417
 Db 898 GCCAGCTCCTCCCTGATCGCCATGCCTCAGTACTTCCACGTGGTGGCGGCACCATTTGA 957
 QY 1418 TTCCTCCAGAGGGGTGCCAGCTGCACGAGTTCCCGCAGTACGTGAAGACGACCTGGCC 1477
 Db 958 TTCGCTCTGAAGGTGGGCAGATCCCAGGCTTCGGGAATTCCTGAAGAAGTCCATCCC 1017
 QY 1478 CTGGCCACCGACC 1490
 Db 1018 AGGAAGTCTGTCC 1030

RESULT 10
 US-09-016-434-1432
 ; Sequence 1432, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1432:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3234 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g599819

US-09-016-434-1432
 Query Match 3.1%; Score 111; DB 4; Length 3234;
 Best Local Similarity 51.7%; Pred. No. 5.2e-13;
 Matches 286; Conservative 0; Mismatches 255; Indels 12; Gaps 1;
 QY 938 CAGGTCAGCTACGGTGTAGCATGGAGCTGTGAGCGCCCGGAGACCTTCCCTCCTTC 997
 Db 490 CAGGTCAGTTATGCCTCCTCCAGCAGACTCCTCAGCAACAAGATCAATTCAAGTCTTC 549

QY 998 TTCCGCACCGTGGCCAGCAGCAGCAGTGTGACGTGACGGCCGCGGAGCTGCTGCAGGAG 1057
 Db 550 CTCCGAACCATCCCAATGATGAGCACCCAGGCCACTGCCATGGCAGACATCATCGAGTAT 609
 QY 1058 TTCGGCTGGAACCTGGTGGCCGCTGGGAGCAGCAGCAGTACGGCCGCGCAGGCGCTG 1117
 Db 610 TTCGGCTGGAACCTGGTGGCACAATTGCGAGCTGATGACGACTATGGCGCGCGGGATT 669
 QY 1118 AGCATCTTCTCGGCCCTGGCCGCGGCACGCGGCATCTGCATCGCGCAGCAGGCGCTGGTG 1177
 Db 670 GAGAAATTCGAGAGGAAGCTGAGGAAAGGATATCTGCATCGACTTCAGTGAACATCATC 729
 QY 1178 CCGCTGCCCGCTGCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCTCTGCACAGGTG 1237
 Db 730 TCCAGTACTCTGATGA-----GGAAGAGATCCAGCATGTGTAGAGGTGATT 777
 QY 1238 AACCAGAGCAGCGTGCAGGTGGTGTGCTGTTCGCTTCCGCTCCGCGCCACGCCCCCTC 1297
 Db 778 CAAAATTCACGGCCAAAAGTCATCGTGGTTTCTCCAGTGGCCAGATCTTGAGCCCCCTC 837
 QY 1298 TTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAAGGTGTGGTGGCCAGGAGGCTTG 1357
 Db 838 ATCAAGGAGATTGTCCGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGCAGGCGCTGG 897
 QY 1358 CTGACCTCTGACCTGGTGTGCGGCTGCGCGCATGGCCAGATGGGCACGCTGTGGC 1417
 Db 898 GCCAGCTCCTCCCTGATGCCATGCCTCAGTACTTCCAGTGGTTGGCGGCACCATTTGA 957
 QY 1418 TTCCTCCAGAGGGGTGCCAGCTGCACGAGTTCCTCCAGTACGTGAAGACGACCTGGCC 1477
 Db 958 TTCGCTCTGAAGGTGGCAGATCCCAGGCTTCGGGAATTCCTGAAGAAGTCCATCCC 1017
 QY 1478 CTGGCCACCGACC 1490
 Db 1018 AGGAAGTCTGTCC 1030

RESULT 11
 US-08-485-588-3
 ; Sequence 3, Application US/08485588
 ; Patent No. 5688938
 ; GENERAL INFORMATION:
 ; APPLICANT: Edward M. Brown
 ; APPLICANT: Steven C. Hebert
 ; APPLICANT: Forrest H. Fuller
 ; APPLICANT: James E. Garrett, Jr.
 ; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 ; TITLE OF INVENTION: MOLECULES
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: First Interstate World Center
 ; STREET: Suite 4700
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FASTSEQ
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,588
 ; FILING DATE: 7 June, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below: 9
 ; APPLICATION NUMBER: 08/353,784
 ; FILING DATE: 9 December, 1994
 ; APPLICATION NUMBER: PCT/US/94/12117


```

/ APPLICANT: Bradford C. Van Wagenen, Manuel
/ APPLICANT: F. Balandrin, Forrest H. Fuller,
/ APPLICANT: Eric G. DelMar, and Scott T. Moe
/ TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
/ TITLE OF INVENTION: MOLECULES
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: First Interstate World Center
/ STREET: Suite 4700
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: FASTSEQ
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/353,784
/ FILING DATE: 9 December, 1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below: 8
/ APPLICATION NUMBER: PCT/US/94/12117
/ FILING DATE: 21 October, 1994
/ APPLICATION NUMBER: U.S. 08/292,827
/ FILING DATE: 23 August, 1994
/ APPLICATION NUMBER: U.S. 08/141,248
/ FILING DATE: 22 October, 1993
/ APPLICATION NUMBER: U.S. 08/009,389
/ FILING DATE: 23 February, 1993
/ APPLICATION NUMBER: U.S. 08/017,127
/ FILING DATE: 12 February, 1993
/ APPLICATION NUMBER: U.S. 07/934,161
/ FILING DATE: 21 August, 1992
/ APPLICATION NUMBER: U.S. 07/834,044
/ FILING DATE: 11 February, 1992
/ APPLICATION NUMBER: U.S. 07/749,451
/ FILING DATE: 23 August, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heber, Sheldon O.
/ REGISTRATION NUMBER: 38,179
/ REFERENCE/DOCKET NUMBER: 209/069
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3809 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 373..3606
/ OTHER INFORMATION:
/
US-08-353-784-3

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Query Match 3.1%; Score 111; DB 3; Length 3809;
Best Local Similarity 51.7%;
Pred. No. 5.4e-13;
Matches 286; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

QY	938	CAGGT	CAGCT	ACGGT	GTCTAG	CATGG	AGAGT	GTCTG	AGCGC	CCCGG	GAGAC	CTTCC	CTCTC	CTTC	997
Db	862	CAGGT <th>CAGT</th> <th>TATGC</th> <th>CTCTCC</th> <th>AGCAG</th> <th>ACTCCT</th> <th>CAGCA</th> <th>CAAGA</th> <th>ATCAAT</th> <th>TCAAG</th> <th>TCTTC</th> <th>CTTC</th> <th>921</th>	CAGT	TATGC	CTCTCC	AGCAG	ACTCCT	CAGCA	CAAGA	ATCAAT	TCAAG	TCTTC	CTTC	921	
QY	998	TTCCG	CACCG	TGCCG	CACCG	CGTGT	GTGCAG	CTGAC	GGCCG	CCGGG	AGCTG	CTGCAG	GAG	105	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:37:08 ; Search time 157 Seconds
(without alignments)
1917.031 Million cell updates/sec

Title: US-10-035-045-21
Perfect score: 4443
Sequence: 1 MGPRAKTICSLFFLLWVLAEE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4443	100.0	839	5	ABB79834 Human tas
2	4443	100.0	839	6	ABP70450 Amino aci
3	4443	100.0	839	8	ADG73580 Human T1R
4	4422	99.5	839	6	ABR43488 Human swe
5	4392.5	98.9	838	7	ADK90719 Human tas
6	3463.5	78.0	669	3	AAY77558 Human GPC
7	3463.5	78.0	669	6	ABP81755 Human G p
8	3231	72.7	843	3	AAY77556 Rat GPCR-
9	3231	72.7	843	6	ABR43494 Rat sweet
10	3231	72.7	843	7	ADK90717 Rat taste
11	3231	72.7	843	8	ADI41010 Rat taste
12	3231	72.7	843	8	ADI40978 Rat taste
13	3179	71.6	843	3	AAY77557 Mouse GPC
14	3179	71.6	843	7	ADK90718 Mouse tas
15	3179	71.6	843	8	ADM42817 Murine ta
16	3179	71.6	843	8	ADP70073 Mouse T1R
17	2532.5	57.0	661	6	ABR43491 Mouse swe
18	1456.5	32.8	840	3	AAY45021 Rat senso
19	1456.5	32.8	840	6	ABR43493 Rat sweet
20	1456.5	32.8	840	7	ADK90711 Rat taste
21	1456.5	32.8	840	7	ADJ93197 Rat taste
22	1456.5	32.8	840	8	ADI40979 Rat taste
23	1456.5	32.8	840	8	ADI41009 Rat taste
24	1455.5	32.8	840	3	AAY45028 Rat senso
25	1454.5	32.7	840	3	AAY45026 Rat senso

26	1453.5	32.7	840	3	AAY45027 Rat senso
27	1446.5	32.6	842	8	ADI40975 Mouse swe
28	1446.5	32.6	842	8	ADI41007 Mouse swe
29	1440.5	32.4	842	3	AAY45022 Mouse sen
30	1440.5	32.4	842	6	ABR43490 Mouse tas
31	1440.5	32.4	842	7	ADK90712 Mouse tas
32	1440.5	32.4	842	8	ADM42819 Murine ta
33	1440.5	32.4	842	8	ADP70072 Mouse T1R
34	1437.5	32.4	842	8	ADI41008 Mouse swe
35	1351.5	30.4	841	4	AAE11969 Human nov
36	1351.5	30.4	841	4	AAE10372 Human tas
37	1351.5	30.4	841	5	ABB77319 Human G-p
38	1351.5	30.4	841	5	ABB79833 Human tas
39	1351.5	30.4	841	6	ABP70449 Amino aci
40	1351.5	30.4	841	7	ADK90736 Human tas
41	1351.5	30.4	841	8	ADG73579 Human T1R
42	1351.5	30.4	841	8	ADM42821 Human tas
43	1350.5	30.4	841	7	ADC26177 Human NOV
44	1334	30.0	840	7	ADK90713 Human tas
45	1289	29.0	929	7	ADC86415 Human GPC

ALIGNMENTS

RESULT 1
ABB79834
ID ABB79834 standard; protein; 839 AA.
XX
AC ABB79834;
XX
DT 25-NOV-2002 (first entry)
XX
DE Human taste cell specific receptor hT1R2.
XX
KW hT1R2; T1R2; T1R; G-protein coupled receptor; receptor; human; taste;
KW sweet.
XX
OS Homo sapiens.
XX
PN WO200264631-A2.
XX
PD 22-AUG-2002.
XX
PF 03-JAN-2002; 2002WO-US000198.
XX
PR 03-JAN-2001; 2001US-0259227P.
PR 19-APR-2001; 2001US-0284547P.
(SENO-) SENOMYX INC.
Adler JE, Li X, Staszewski L, O'connell S, Zozulya S;
WPI; 2002-666991/71.
DR N-PSDB; ABN84928.
XX
PT Novel mammalian taste-cell specific G protein-coupled receptors active in
taste signaling, useful for representing the perception of taste and for
predicting the perception of taste in a mammal.
PS Claim 152; Page 90; 132pp; English.
XX
CC The present sequence is the protein sequence of a novel human G-protein
coupled receptor (GPCR), designated hT1R2, that is involved in sweet
taste transduction. The invention provides a new family of taste cell-
specific GPCRs, the T1Rs, active in taste perception. Genomic DNAs and
cDNAs encoding the receptors are described, along with methods for
isolating T1R genes and for isolating and expressing T1R polypeptides.
CC Methods for representing taste perception of a particular taste stimulus
in a mammal, including a human, are also described, as are methods for
generating novel molecules or combinations of molecules that elicit a
predetermined taste perception in a mammal, and methods for stimulating
one or more tastes. Methods for stimulating or blocking taste perception

CC are also disclosed, as are methods of screening for modulators of these
CC novel taste cell-specific GPCRs. Such modulators are useful for
CC pharmacological, chemical and genetic modulation of taste signalling
CC pathways. They can be used in the food or pharmaceutical industries to
CC customize taste, e.g. to modulate the sweet tastes of foods or drugs. T1R
CC proteins and polypeptides are useful for identifying taste cells present
CC in the oral cavity, gastrointestinal epithelium and epiglottis. They may
CC also serve as tools for the generation of taste topographic maps that
CC elucidate the relationship between the taste cells of the tongue and
CC taste sensory neurons leading to taste centres in the brain
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4443; DB 5; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLQVPMCK 60
Db 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLQVPMCK 60
QY 61 EYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120
Db 61 EYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120
QY 121 LLPIQEDYSNYSRVVAVIGPDNSESVMVTANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db 121 LLPIQEDYSNYSRVVAVIGPDNSESVMVTANFLSLFLLPQITYSAISDELDRKVRFPAL 180
QY 181 LRTTPSADHHVEAMVQMLHFRWNWIIIVLVSDDTYGRDNGQLLGERVARRDICIAFQETL 240
Db 181 LRTTPSADHHVEAMVQMLHFRWNWIIIVLVSDDTYGRDNGQLLGERVARRDICIAFQETL 240
QY 241 PTLQPNQNMTEERQRLVTIVDKLQQSTARVVVVFSPDLTYLHFFNEVLQNFAGVWIA 300
Db 241 PTLQPNQNMTEERQRLVTIVDKLQQSTARVVVVFSPDLTYLHFFNEVLQNFAGVWIA 300
QY 301 SESWAIDPVLHNLTELGLGTFLGITIQQSVPIPGFSEFREWGPAGPPPLSRTSQSYTCN 360
Db 301 SESWAIDPVLHNLTELGLGTFLGITIQQSVPIPGFSEFREWGPAGPPPLSRTSQSYTCN 360
QY 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVPWQL 420
Db 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVPWQL 420
QY 421 LEEIWKVNFTLLDHIQIFFDPQGDVALHLEIVQWQDRSONPFQSVASYPLQRLKNIQD 480
Db 421 LEEIWKVNFTLLDHIQIFFDPQGDVALHLEIVQWQDRSONPFQSVASYPLQRLKNIQD 480
QY 481 ISWHTVNNNTIPIVMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTVNNNTIPIVMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
Db 601 GPMCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
QY 661 MASRFPFRAYSYWRYQGPVYSMAFITVLKMWIVIGMLATGLSPTRTDPDPKITIVSC 720
Db 661 MASRFPFRAYSYWRYQGPVYSMAFITVLKMWIVIGMLATGLSPTRTDPDPKITIVSC 720
QY 721 NPNYRNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFFYTSVSLCTFM 780
Db 721 NPNYRNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFFYTSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVINLLAISLGYFGPKCYMILFYPERNTPAYFNSMTQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVINLLAISLGYFGPKCYMILFYPERNTPAYFNSMTQGYTMRD 839

RESULT 2
ABP70450
ID ABP70450 standard; protein; 839 AA.
XX
AC ABP70450;
XX
DT 22-APR-2003 (first entry)
XX
DE Amino acid sequence of human T1R2.
XX
KW T1 receptor; T1R3; G protein-coupled receptor; GPCR; T1R2; T1R3;
KW sweet taste stimuli; T1R2; umami taste stimuli; taste stimuli;
KW taste perception; taste sensation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 221
FT /note= "Gln encoded by AG"
XX
PN WO2003001876-A2.
XX
PD 09-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-US019970.
XX
PR 26-JUN-2001; 2001US-0300434P.
PR 03-JUL-2001; 2001US-00897427.
PR 13-JUL-2001; 2001US-0304749P.
PR 08-AUG-2001; 2001US-0310493P.
PR 21-NOV-2001; 2001US-0331771P.
PR 14-DEC-2001; 2001US-0339472P.
PR 03-JAN-2002; 2002US-00035045.
PR 15-APR-2002; 2002US-0372090P.
PR 22-APR-2002; 2002US-0374143P.
XX
(SENO-) SENOMYX INC.
XX
PI Zoller MT, Li X, Staszewski L, O'Connell S, Zozulya S, Adler JE;
PI Xu H, Echeverri F;
XX
DR WPI; 2003-210181/20.
DR N-PSDB; ABZ68279.
XX
PT New receptor that comprises T1R1 and/or T1R3 or T1R2 and/or T1R3
PT polypeptide and that specifically binds to and/or is activated by umami
PT or sweet taste stimuli, useful for identifying compounds that modulate
PT taste perception.
XX
XX Example 1; Page 80; 135pp; English.
XX
CC The present sequence represents a human T1 receptor designated T1R2. The
CC receptor is a G protein-coupled receptor (GPCR). T1R2 and T1R3 act in
CC combination to recognise sweet taste stimuli, while T1R2 and T1R3 act in
CC combination to recognise umami taste stimuli. The specification describes
CC different combinations of T1Rs, that when co-expressed, produce
CC functional taste receptors that respond to taste stimuli. The hetero-
CC oligomeric taste receptors of the invention are useful for identifying
CC compounds that modulate taste perception. They are also useful for
CC modifying taste sensation in an animal
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4443; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLQVPMCK 60
Db 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLQVPMCK 60
QY 61 EYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120

Db 61 EYEKVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCISNNVQPVLYFLAHEDN 120
QY 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
QY 181 LRTTPSADHHVEAMVQLMLHFRWNIIIVLVSSDYGNDGQLLGERVARRDICIATQETL 240
Db 181 LRTTPSADHHVEAMVQLMLHFRWNIIIVLVSSDYGNDGQLLGERVARRDICIATQETL 240
QY 241 PTLQPNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTYHFFNEVLRQNTGAVWIA 300
Db 241 PTLQPNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTYHFFNEVLRQNTGAVWIA 300
QY 301 SESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db 301 SESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECNCLNATLSFNTILRSGERVVYSVAVYAVAHALHSLGCDKSTCTKRVPVVPWQL 420
Db 361 QECNCLNATLSFNTILRSGERVVYSVAVYAVAHALHSLGCDKSTCTKRVPVVPWQL 420
QY 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWDRSQNPFSQSVASYPLQRLKNIQD 480
Db 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWDRSQNPFSQSVASYPLQRLKNIQD 480
QY 481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYBCQACP 540
Db 481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYBCQACP 540
QY 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFMLMTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISIAVRSFOIVCAFK 660
Db 601 GPMCFMLMTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISIAVRSFOIVCAFK 660
QY 661 MASRFPRAYSYVWRVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPPDKITIVSC 720
Db 661 MASRFPRAYSYVWRVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPPDKITIVSC 720
QY 721 NPNYRNSLLENTSLDLLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
Db 721 NPNYRNSLLENTSLDLLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 3
ADG73580
ID ADG73580 standard; protein; 839 AA.

XX AC ADG73580;

XX DT 11-MAR-2004 (first entry)

XX DE Human T1R2.

XX KW umami receptor; sweet taste receptor; taste perception; food; beverage;
XX KW umami; sweet taste; human.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 221

FT /note= "Encoded by AG"

FT Misc-difference 696

FT /note= "Encoded by GGC"

PN US2003232407-A1.
XX 18-DEC-2003.
PD 26-JUN-2002; 2002US-00179373.
XX 26-JUN-2001; 2001US-0300434P.
PR 13-JUL-2001; 2001US-0304749P.
PR 08-AUG-2001; 2001US-0310493P.
PR 21-NOV-2001; 2001US-0331771P.
PR 14-DEC-2001; 2001US-0339472P.
PR 15-APR-2002; 2002US-0372090P.
PR 22-APR-2002; 2002US-0374143P.
PR 23-APR-2002; 2002US-0374522P.
XX (SENO-) SENOMYX INC.

PA Zoller M, Li X, Staszewski L, O'connell S, Zozulya S, Adler JE;

XX Xu H, Echeverri F;

PI WPI; 2004-052170/05.

XX N-PSDB; ADG73584.

Novel receptors T1R1 and T1R3 that respond to umami taste stimuli and receptors T1R2 and T1R3 that respond to sweet taste stimuli, useful for identifying modulators which are used for modifying taste sensation in animals.

Example 1; SEQ ID NO 6; 55pp; English.

The invention relates to a receptor comprised of at least one T1R1 polypeptide and/or at least one T1R3 polypeptide or a receptor comprised of at least one T1R2 polypeptide and/or at least one T1R3 polypeptide where the receptors specifically bind to and/or are activated by umami or sweet taste stimuli. The receptor is useful for identifying compounds that modulate taste perception, where the method involves identifying compounds that bind to, activate, inhibit, enhance and/or modulate one or more of the receptors. The receptor is useful for quantifying the taste of individual compounds or food or beverage compositions. The method is used to screen a compound library for compounds that enhance or modulate the activity of L-glutamate to activate the T1R1/T1R3 umami taste receptor, or to screen a compound library for compounds that agonise or antagonise the T1R1/T1R3 sweet taste receptor. The method screens for a compound that competes with IMP, GMP or their analogues for binding to the T1R1/T1R3 umami taste receptor. The method is used to screen a compound library for compounds that mimic the activity of IMP, GMP or their analogues that enhance the activity of a T1R1/T1R3 agonist or is used to screen a compound library for compounds that enhance or modulate the activity of a sweetener to activate the T1R2/T1R3 sweet taste receptor. The method is useful for modifying umami taste or sweet taste sensation in an animal such as human, dog, cat, fish, cow, sheep or pig. The compound is formulated in a food, beverage, or oral pharmaceutical composition. The present sequence represents the amino acid sequence of human T1R2.

XX SQ Sequence 839 AA;

Query Match 100.0%; Score 4443; DB 8; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
Db 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
QY 61 EYEVKVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCISNNVQPVLYFLAHEDN 120
Db 61 EYEVKVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCISNNVQPVLYFLAHEDN 120
QY 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICIATQETL 240
Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICIATQETL 240
QY 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA 300
Db 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA 300
QY 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVVAHAHSLGCDKSTCTKRVPWQ 420
Db 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVVAHAHSLGCDKSTCTKRVPWQ 420
QY 421 LEEIWKVNFLLDHQIIFDDPQGDVALHLEIVQWQDRSQNPFFQSVASYPLQRLKNIQD 480
Db 421 LEEIWKVNFLLDHQIIFDDPQGDVALHLEIVQWQDRSQNPFFQSVASYPLQRLKNIQD 480
QY 481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFMLTLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660
Db 601 GPMCFMLTLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660
QY 661 MASRFPRAYSYWVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPDDPKITIVSC 720
Db 661 MASRFPRAYSYWVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPDDPKITIVSC 720
QY 721 NPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db 721 NPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 4
ABR43488
ID ABR43488 standard; protein; 839 AA.

AC ABR43488;

DT 21-JUL-2003 (first entry)

DE Human sweet taste receptor TIR2 protein SEQ ID NO:4.

KW Human; sweet taste receptor; TIR1; TIR2; TIR3; gene therapy;
KW tasting defect; taste discrimination; chromosome 1.

OS Homo sapiens.

PN WO2003025137-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-US029449.

PR 18-SEP-2001; 2001US-0323450P.

XX (IRMI-) IRM LLC.

PA (SCRI) SCRIPPS RES INST.

PI Liao J, Ding S, Schultz PG;

XX

DR WPI; 2003-363139/34.
DR N-PSDB; ACC69593.

XX
PT New human sweet receptor gene, useful for preparing a composition for
treating tasting defects or for enhancing taste discrimination.

XX
PS Claim 1; Page 61; 80pp; English.

XX
CC The present invention describes human, mouse and rat sweet taste
receptors TIR1, TIR2 and TIR3. Human sweet taste receptors are located on
chromosome 1, and mouse sweet taste receptors are located on chromosome
4. The sweet taste receptors can be used in gene therapy. They can also
be used for preparing a composition for treating defects or for
enhancing taste discrimination. The present sequence represents human
TIR2, which is given in the exemplification of the present invention

XX
SQ Sequence 839 AA;

Query Match 99.5%; Score 4422; DB 6; Length 839;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 834; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFFLLWVLAEPANSDYLPDGYLLGGLPSLHANMKGIVHLNPLQVPMCK 60

Db 1 MGPRAKTICSLFFLLWVLAEPANSDYLPDGYLLGGLPSLHANMKGIVHLNPLQVPMCK 60

QY 61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120

Db 61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAHEDN 120

QY 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180

Db 121 LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICIATQETL 240

Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICIATQETL 240

QY 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA 300

Db 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIA 300

QY 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360

Db 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360

QY 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVVAHAHSLGCDKSTCTKRVPWQ 420

Db 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVVAHAHSLGCDKSTCTKRVPWQ 420

QY 421 LEEIWKVNFLLDHQIIFDDPQGDVALHLEIVQWQDRSQNPFFQSVASYPLQRLKNIQD 480

Db 421 LEEIWKVNFLLDHQIIFDDPQGDVALHLEIVQWQDRSQNPFFQSVASYPLQRLKNIQD 480

QY 481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540

Db 481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540

QY 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600

Db 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600

QY 601 GPMCFMLTLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660

Db 601 GPMCFMLTLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660

QY 661 MASRFPRAYSYWVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPDDPKITIVSC 720

Db 661 MASRFPRAYSYWVRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTRTDPDDPKITIVSC 720

QY 721 NPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780

Db 721 NPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780

QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 839
Db |||||
781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 839

RESULT 5
ADK90719
ID ADK90719 standard; protein; 838 AA.
XX
AC ADK90719;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human taste receptor T1R2 protein.
XX
KW gene therapy; taste receptor; T1R3; T1R1; T1R2; taste-induced behavior;
KW taste topographic map; tongue; taste cell; taste sensory neuron;
KW brain taste center.
XX
OS Homo sapiens.
XX
PN WO2003004992-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US021269.
XX
PR 03-JUL-2001; 2001US-0302898P.
PR 10-AUG-2001; 2001US-00927315.
PR 22-FEB-2002; 2002US-0358925P.
XX
XX (REGC) UNIV CALIFORNIA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Zuker CS, Ryba NJP, Chandrashekar J, Hoon MA, Nelson GA, Zhang Y;
XX
DR WPI; 2003-210382/20.
DR N-PSDB; ADK90722.
XX
PT New taste receptors comprising a T1R3 polypeptide and optionally a T1R1
PT or T1R2 polypeptide, useful as probes for identifying taste cells; and in
PT gene therapy for correcting acquired and inherited genetic defects.
XX
PS Claim 22; SEQ ID NO 9; 119pp; English.
XX
CC The invention relates to a novel taste receptor comprising a T1R3
CC polypeptide and optionally a T1R1 or T1R2 polypeptide. The nucleic acids
CC and proteins encoding the receptors may be used as probes to identify
CC taste cells or subsets of taste cells or to dissect taste-induced
CC behaviors, and in the generation of taste topographic maps that elucidate
CC the relationship between the taste cells of the tongue and taste sensory
CC neurons leading to taste centers in the brain. Nucleic acids encoding T1R
CC protein can be used with highly density oligonucleotide array technology
CC to identify T1R protein, orthologs, alleles, conservatively modified
CC variants, and polymorphic variants in this invention. The nucleic acids
CC may be inserted into vectors for gene therapy correct acquired and
CC inherited genetic defects and other diseases. Compositions may be
CC administered to elicit a therapeutic response in the patient. Modulators
CC of sweet and/or amino acid taste transduction are useful for
CC pharmacological and genetic modulation of sweet and amino acid taste
CC ligands, and in food and pharmaceutical industries to customize taste.
CC This sequence corresponds to the human T1R2 protein.
XX
SQ Sequence 838 AA;

Query Match 98.9%; Score 4392.5; DB 7; Length 838;
Best Local Similarity 99.3%; Pred. NO. 0;
Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MGPRAKTICSLFFLLWVLAEPANSDFYLPDGYLLGGLFSLHANKGIVHLNFLQVPMCK 60
Db |||||
1 MGPRAKTICSLFFLLWVLAEPANSDFYLPDGYLLGGLFSLHANKGIVHLNFLQVPMCK 60

QY 61 EYEVKVI GYNLMQAMRF AVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db |||||
61 EYEVKVI GYNLMQAMRF AVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120

QY 121 LLPIQEDYSNIYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL 180
Db |||||
121 LLPIQEDYSNIYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL 180

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICI AFQETL 240
Db |||||
181 LRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICI AFQETL 240

QY 241 PTLQPNQNTSEERQLVTIVDKLQOSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIA 300
Db |||||
241 PTLQPNQNTSEERQLVTIVDKLQOSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIA 300

QY 301 SESWAIDPVLHNLTELGHGLTGFLGTTIQSVPIPGFSEFEWGPQAGPPPLSRTSQSYTCN 360
Db |||||
301 SESWAIDPVLHNLTELGHGLTGFLGTTIQSVPIPGFSEFEWGPQAGPPPLSRTSQSYTCN 360

QY 361 QECDNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLLGCDKSTCTKRVPVYPWL 420
Db |||||
361 QECDNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLLGCDKSTCTKRVPVYPWL 420

QY 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFOQSVASYYPQLQRLKNIQD 480
Db |||||
421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFOQSVASYYPQLQRLKNIQD 480

QY 481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGFLNHTEDEYECQACPN 540
Db |||||
481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGFLNHTEDEYECQACPN 540

QY 541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSTLAILVFWRHFTPIVRSAG 600
Db |||||
541 NEWSYQSETSCFKRQLVFLWEHAPTIAVALLAALGFLSTLAILVFWRHFTPIVRSAG 600

QY 601 GPMCFLMLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTTICISCIARSFQIVCAFK 660
Db |||||
601 GPMCFLMLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFTTICISCIARSFQIVCAFK 660

QY 661 MASRFRAYSWVRYQGPVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
Db |||||
661 MASRFRAYSWVRYQGPVSMAFITVLKMWIVVIGMLARPOS-HPRTPDDPKITIVSC 719

QY 721 NPVNRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFFYFTSSVSLCTFM 780
Db |||||
720 NPVNRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFFYFTSSVSLCTFM 779

QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 839
Db |||||
780 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 838

RESULT 6
AAY77558
ID AAY77558 standard; protein; 669 AA.
XX
AC AAY77558;
XX
DT 08-MAY-2000 (first entry)
XX
DE Human GPCR-B4 polypeptide.
XX
KW Sensory transduction G-protein coupled receptor; GPCR; GPCR-B4; human;
KW taste transduction pathway; taste receptor; foliate; fungiform; food;
KW circumvallate; taste signaling; pharmaceutical.
OS Homo sapiens.
XX
PN WO200006593-A1.
XX
PD 10-FEB-2000.

XX 27-JUL-1999; 99WO-US017104.

PR 28-JUL-1998; 98US-0095464P.

PR 17-DEC-1998; 98US-0112747P.

XX (REGC) UNIV CALIFORNIA.

XX Zuker CS, Adler JE, Lindemeier J;

XX WPI; 2000-195257/17.

DR N-PSDB; AAZ58965.

XX New isolated sensory transduction G-protein coupled receptor, useful for

PT developing products for use in studying and modulating the taste

PT transduction pathway and for generating taste topographic maps.

XX Claim 22; Page 73; 76pp; English.

XX The invention provides nucleic acids encoding rat, mouse and human

CC sensory transduction G-protein coupled receptor (GPCR) polypeptides. The

CC GPCR polypeptides are components of the taste transduction pathway. The

CC nucleic acids can be used to identify taste cells and as tools for the

CC generation of taste topographic maps that elucidate the relationship

CC between the taste cells of the tongue and taste sensory neurons leading

CC to taste centers in the brain. GPCR-B4 is useful as a nucleic acid probe

CC for identifying subpopulations of taste receptor cells such as foliate,

CC fungiform, and circumvallate taste receptor cells. The polypeptides can

CC be used for identifying compounds that modulate sensory signaling in

CC sensory cells. Such modulators of taste transduction are useful for

CC pharmacological and genetic modulation of taste signaling pathways. These

CC modulatory compounds can then be used in the food and pharmaceutical

CC industries to customize taste. The present sequence represents a human

CC GPCR-B4 polypeptide

XX Sequence 669 AA;

Query Match 78.0%; Score 3463.5; DB 3; Length 669;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY 162 ITYSAISDELKRVFPALLRTPPSADHHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQ 221

Db 1 ITYSAISDELKRVFPALLRTPPSADHHVEAMVQLMLHFRWNIIIVLVSSDTYGRDNGQ 60

QY 222 LLGERVARRDICIATFQETLPTLPQNQNMTSEERQRLVITVDKLQOSTARVVVFPSPDLTL 281

Db 61 LLGERVARRDICIATFQETLPTLPQNQNMTSEERQRLVITVDKLQOSTARVVVFPSPDLTL 120

QY 282 YHFFNEVLNQFTGAVWIASESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGSEFREW 341

Db 121 YHFFNEVLNQFTGAVWIASESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGSEFREW 180

QY 342 GPQAGPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGERVVSVYSAVVAHALHS 401

Db 181 GPQAGPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGERVVSVYSAVVAHALHS 240

QY 402 LLGCDKSTCTKRVVYPWQLLEEIKVNFLLDQIFFPDQGDVALHLEIVQWQWDRSQNP 461

Db 241 LLGCDKSTCTKRVVYPWQLLEEIKVNFLLDQIFFPDQGDVALHLEIVQWQWDRSQNP 300

QY 462 FQSVASYPLQRLQNIQDISWHTVNNTPMSMCKRCQSGQKKKPVGIHVCCECIDCL 521

Db 301 FQSVASYPLQRLQKNIK-TSLHTVNNTPMSMCKRCQSGQKKKPVGIHVCCECIDCL 359

QY 522 PGTFLNHTEDEYECQACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTL 581

Db 360 PGTFLNHTE-----CPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTL 412

QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLTLLVAYMVVVPVVGPPKVVSTCLCRQALFPLCF 641

Db 413 AILVIFWRHFQTPIVRSAGGPMCFMLTLTLLVAYMVVVPVVGPPKVVSTCLCRQALFPLCF 472

QY 642 TICISCIATVRSFQIVCAFKMASRFPRAYSWVRYQGPYVSMATITVLKMWIVVIGMLATG 701

Db 473 TICISCIATVRSFQIVCAFKMASRFPRAYSWVRYQGPYVSMATITVLKMWIVVIGMLARP 532

QY 702 LSPTRTRDPDPDKITIVSCNPNYRNSLLFNFTSLDLLLSVVGFSAFYMKGKELPTNYNEAKF 761

Db 533 QS-HPRTPDPDPDKITIVSCNPNYRNSLLFNFTSLDLLLSVVGFSAFYMKGKELPTNYNEAKF 591

QY 762 ITLSMTFFYFTSSVSLCTFMSAYSGLVLTIVDILLVTLNLLAISLGYFGPKCYMILFYPER 821

Db 592 ITLSMTFFYFTSSVSLCTFMSAYSGLVLTIVDILLVTLNLLAISLGYFGPKCYMILFYPER 651

QY 822 NTPAYFNMIQGYTMRRD 839

Db 652 NTPAYFNMIQGYTMRRD 669

RESULT 7

ABP81755

ID ABP81755 standard; protein; 669 AA.

XX ABP81755;

XX 04-MAR-2003 (first entry)

XX Human G protein-coupled receptor GPCR4 protein SEQ ID NO:683.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

PD 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

PF 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

DR New isolated antigenic peptides e.g., for G protein-coupled receptors

XX (GPCR), useful for diagnosing and designing drugs for treating conditions

PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

PS The present invention describes antigenic peptides (I) comprising: (a)

XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular G

CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity or

CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in

CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

CC antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the

CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 669 AA;

Query Match 78.0%; Score 3463.5; DB 6; Length 669;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY 162 ITYSAISDELKDKVFPALLRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQ 221
Db 1 ITYSAISDELKDKVFPALLRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQ 60
QY 222 LLGERVARRDICIARQETLPTLOPNQNTSEERQRLVTIVDKLQOSTARVVVFPDRTL 281
Db 61 LLGERVARRDICIARQETLPTLOPNQNTSEERQRLVTIVDKLQOSTARVVVFPDRTL 120
QY 282 YHFFNEVLQRNFTGAVWIASWADPVLHNLTELGLGTFLGITIQSVPIPGFSEFREW 341
Db 121 YHFFNEVLQRNFTGAVWIASWADPVLHNLTELGLGTFLGITIQSVPIPGFSEFREW 180
QY 342 GPQAGPPPLSRTSQTNCQECNCLNATLSFNTILRLSGERVVSVYSAVVAHALHS 401
Db 181 GPQAGPPPLSRTSQTNCQECNCLNATLSFNTILRLSGERVVSVYSAVVAHALHS 240
QY 402 LLGCDKSTCTKRVVYPWQLLEEIKVKNFTLLDQIIFDPPQGDVALHLEIVQWQDRSQNP 461
Db 241 LLGCDKSTCTKRVVYPWQLLEEIKVKNFTLLDQIIFDPPQGDVALHLEIVQWQDRSQNP 300
QY 462 FQSVASYYPQLRQKNIQDISWHTVNTIPMSCKSRQSQGKKPVGIVHCCFECIDCL 521
Db 301 FQSVASYYPQLRQKNIK-TSLHTVNTIPMSCKSRQSQGKKPVGIVHCCFECIDCL 359
QY 522 PGTFNLNHTEDYECQACPNNEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTL 581
Db 360 PGTFNLNHTEDYECQACPNNEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTL 412
QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLLVAYMVVPVYVGPVKVSTCLCRQALFPLCF 641
Db 413 AILVIFWRHFQTPIVRSAGGPMCFMLTLLVAYMVVPVYVGPVKVSTCLCRQALFPLCF 472
QY 642 TICISCIARVSFQIVCAFKMASRFRAYSVWVYQGPYVSMAFITVLKMWIVVIGMLATG 701
Db 473 TICISCIARVSFQIVCAFKMASRFRAYSVWVYQGPYVSMAFITVLKMWIVVIGMLARP 532
QY 702 LSPTRTRDPPDKITIVSCNPNYRNSLLFNTSLDLLSVVGFSFAYMGKELPTNYNEAKF 761
Db 533 QS-HPRTDPPDKITIVSCNPNYRNSLLFNTSLDLLSVVGFSFAYMGKELPTNYNEAKF 591
QY 762 ITLSMTFTYSSVSLCTFMSAYSGLVTIVDILLVTLNLLAISLGFGPKCYMILFYPER 821
Db 592 ITLSMTFTYSSVSLCTFMSAYSGLVTIVDILLVTLNLLAISLGFGPKCYMILFYPER 651
QY 822 NTPAYFNSMIQGYTMRD 839
Db 652 NTPAYFNSMIQGYTMRD 669

RESULT 8
AA77556
ID AA77556 standard; protein; 843 AA.

XX
AC AAY77556;
XX 08-MAY-2000 (first entry)
DT Rat GPCR-B4 polypeptide.
DE
XX Sensory transduction G-protein coupled receptor; GPCR; GPCR-B4; rat;
KW taste transduction pathway; taste receptor; foliate; fungiform; food;
KW circumvallate; taste signaling; pharmaceutical.
XX Rattus sp.
OS
XX WO200006593-A1.
PN
XX 10-FEB-2000.
PD
XX 27-JUL-1999; 99WO-US017104.
PF
XX 28-JUL-1998; 98US-0095464P.
PR 17-DEC-1998; 98US-0112747P.
XX (REGC) UNIV CALIFORNIA.
PI Zuker CS, Adler JE, Lindemeier J;
XX WPI; 2000-195257/17.
DR N-PSDB; AAZ58963.
XX New isolated sensory transduction G-protein coupled receptor, useful for
PT developing products for use in studying and modulating the taste
PT transduction pathway and for generating taste topographic maps.
XX
PS Claim 22; Page 69; 76pp; English.
XX The invention provides nucleic acids encoding rat, mouse and human
CC sensory transduction G-protein coupled receptor (GPCR) polypeptides. The
CC GPCR polypeptides are components of the taste transduction pathway. The
CC nucleic acids can be used to identify taste cells and as tools for the
CC generation of taste topographic maps that elucidate the relationship
CC between the taste cells of the tongue and taste sensory neurons leading
CC to taste centers in the brain. GPCR-B4 is useful as a nucleic acid probe
CC for identifying subpopulations of taste receptor cells such as foliate,
CC fungiform, and circumvallate taste receptor cells. The polypeptides can
CC be used for identifying compounds that modulate sensory signaling in
CC sensory cells. Such modulators of taste transduction are useful for
CC pharmacological and genetic modulation of taste signaling pathways. These
CC modulatory compounds can then be used in the food and pharmaceutical
CC industries to customize taste. The present sequence represents a rat GPCR
CC -B4 polypeptide
XX
SQ Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 3; Length 843;
Best Local Similarity 70.8%; Pred. No. 1.9e-299;
Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFLLWVLAEP---AENSDFYLPDYLGLGFLSHANMKGIVHLNQLQVP 57
Db 1 MGQPARTLCLLSLLHVLKPKGLVENSDFHLAGDYLGLGFLSHANVKSISHLSYLQVP 60
QY 58 MCKEYEVKVGYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNVQPVLYFLAH 117
Db 61 KCNEFTMKVLYGNLMQAMRFAVEEINNCSLLPGVLLGYEIVDVCYISNNIHPGLYFLAQ 120
QY 118 EDNLLPIQEDYSNYSRNVAVIGPDNSESVMVTVANFLSLFLLPQITYSAISDELKDKVRE 177
Db 121 DDDLLPILKDYSQYMPHVAVIGPDNSESAITVSNILSHFLIPQITYSAISDKLRDKRH 180
QY 178 PALLRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVAR-RDICIAT 236
Db 181 PSMRLTVPSATHHIEAMVQLMVHFQWNWIVLVSSDDYGRNSHLLSQRLLTKTSIDCIAT 240

Db 781 CTFMSVHDGVLVTIMDLLVTNLAIGLGYFGPKCYMILFYPERNTSAVFNSMIQGYTM 840

QY 837 RR 838

Db 841 RK 842

RESULT 12

ADI40978

ID ADI40978 standard; protein; 843 AA.

XX ADI40978;

AC ADI40978;

XX 22-APR-2004 (first entry)

XX Rat taste receptor TR2.

DE

XX Receptor; GPCR; G protein-coupled receptor; reproductive disorder;

KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;

KW XX male; epididymitis; cryptorchidism; sperm transport disorder;

KW testicular cancer; testicular germ cell tumour; male hormone disorder;

KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;

KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;

KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;

KW graft-versus-host disease; autoimmunity disorder;

KW systemic lupus erythematosus; drug induced haemolytic anaemia;

KW Sjogren's disease; T-cell maturation disorder;

KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;

KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;

KW pulmonary disorder; brain disorder; endocrine disorder; cancer;

KW gene therapy.

XX

OS Rattus norvegicus.

XX

PN US2004018976-A1.

XX

XX 29-JAN-2004.

PD

XX

PF 13-MAY-2003; 2003US-00436715.

XX

PR 14-MAY-2002; 2002US-0380336P.

XX

PA (FEDE/) FEDER J N.

PA (MINT/) MINTIER G.

PA (RAMA/) RAMANATHAN C S.

XX

PI Feder JN, Mintier G, Ramanathan CS;

XX WPI; 2004-122081/12.

XX

PT New human G-protein coupled receptor polypeptide and polynucleotide,

PT useful for diagnosing, preventing, treating or ameliorating a medical

PT condition, e.g. reproductive disorder, immunodeficiency disease or

PT testicular cancer.

XX

PS Disclosure; SEQ ID NO 38; 290pp; English.

XX

CC The invention relates to an isolated human G protein-coupled receptor

CC polypeptide and its encoding polynucleotide, including the full length

CC proteins minus the start methionine (and the region of the polynucleotide

CC encoding this protein region). The proteins are designated HGPRBM30-1,

CC HGPRBM30-2, HGPRBM30-3, HGPRBM41-1, HGPRBM41-2, HGPRBM41-3,

CC HGPRBM42, HGPRBM42-1, HGPRBM43 and HGPRBM44. Also included are

CC expression vectors, host cells, antibodies, preventing (treating or

CC ameliorating) a medical condition comprising administering to a mammalian

CC subject the polypeptide or its modulator and diagnosing a pathological

CC condition or a susceptibility to a pathological condition in a subject

CC (comprising determining the presence or absence of a mutation in the

CC polynucleotide, or the presence or amount of expression of the

CC polypeptide in a biological sample and diagnosing a pathological

CC condition or a susceptibility to a pathological condition based on the

CC presence or absence of the mutation, or the presence or amount of

CC expression of the polypeptide). The human G-protein coupled receptor

CC polypeptide or polynucleotide can be used for diagnosing a pathological

CC condition or a susceptibility to a pathological condition in a subject,

CC and for preventing, treating or ameliorating a medical condition, such as

CC a disorder related to aberrant G-protein coupled receptor activity, a

CC disorder related to aberrant signal transduction, a reproductive disorder

CC ; a male reproductive disorder, a testicular disorder, a vas deferens

CC disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,

CC epididymitis, genital warts, germinal cell aplasia, cryptorchidism,

CC varicocele, immotile cilia syndrome, viral orchitis, sperm transport

CC disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,

CC testicular germ cell tumours, male hormone disorders, premature puberty,

CC incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune

CC disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,

CC immunodeficiency diseases such as AIDS, rheumatoid arthritis,

CC granulomatous disease, inflammatory bowel disease, sepsis, acne,

CC neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell

CC mediated cytotoxicity, immune reactions to transplanted organs and

CC tissues, such as host-versus-graft and graft-versus-host diseases, or

CC autoimmunity disorders, such as autoimmune infertility, demyelination,

CC systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's

CC disease, scleroderma, T-cell maturation disorders, B-cell maturation

CC disorders, vascular disorders, stroke, ischaemia, myocardial infarction,

CC atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,

CC irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,

CC endocrine disorders, or ovarian, stomach, colon or kidney cancer or its

CC related proliferative condition (many other diseases and disorders are

CC listed in the specification). The antibodies may be used to purify,

CC detect and target the G-protein coupled receptor polypeptides. The

CC polynucleotides are also useful in gene therapy. The present sequence

CC represents a species homologue of a novel GPCR of the invention.

XX

SQ Sequence 843 AA;

Query Match 72.7%; Score 3231; DB 8; Length 843;

Best Local Similarity 70.8%; Pred. No. 1.9e-299;

Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFELLWLAEP--AENSDFVLPDYLGLGFLSHANMKGIIVHLNQLQVP 57

Db 1 MGPOARTLCLLSLLHVLKPKGLVENSDFHLADYLLGGLFTLHANVKSISHLSYLOVP 60

QY 58 MCKEYEVKVIQYVNLQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAH 117

Db 61 KCNEFTMKVGLGYNLQAMRFAVEEINNCSSLLPGVLLGYEMVDVCYLSNNHPLGLYFLAQ 120

QY 118 EDNLLPIQEDYSYISRVVAVIGPDNSEVMTVANFLSLFLLPQITYSALSDELDRKVR 177

Db 121 DDDLPLPKDYQYMPHVAVIGPDNSESAITVSNILSHFLIPQITYSALSDELDRKVR 180

QY 178 PALLRTTPSADHHVEAMVQLMHLFRWNWIIVLVSSDTYGRDNGQLLGERVAR-RDICI 236

Db 181 PSMRLTPVPSATHIEAMVQLMVFQWNIIVLVSDDDYGRNSHLLSRLTKTSDICIAF 240

QY 237 QETLPTLQPNQNTSEERQLVTIVDKLQOSTARVVVVFSPDLTLVHFFNEVLRQNFTGA 296

Db 241 QEVLPPESSQVVRSEERQLDNLIDKLRTSARVVVVFSPDLTLVHFFNEVLRQNFTGF 300

QY 297 VWIASESWAIDPVHLNLTGLHGLTGITIGTQSVPIPGSEFREWGPQAGPPPLSRTSQS 356

Db 301 VWIASESWAIDPVHLNLTGLHGLTGITIGTQSVPIPGSEFREWGPQAGPPPLSRTNLR 360

QY 357 YTCNQECNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVVY 416

Db 361 TTCNQDCDACLTNTKSFNNILSGERVVYSVAVYVAHALHSLGCDKSTCTKRVVY 420

QY 417 PWQLLEEIKVNFNTLLDHOIFFDPQGDVALHLEIVQWQWDRSQNPFOVSAYYPLQRLK 476

Db 421 PWQLLEIWHVNFNTLLGNRLFFDQDQGMPLLDIIQWQWDLNQNPFOVSAYYPLQRLT 480

QY 477 NIQDISWHTVNTPIPMSCSKRCQSGQKKPVGIHVCCFECIDCLPLGFLNHTDEYECQ 536

Db 481 YINNVSWYTPNTVPMSCSKRCQSGQKKPVGIHVCCFECIDCLPMGTYLNRSADEFNCL 540

QY 121 LLPIQEDYSNISRVAVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPA 180
Db 121 LLPIQEDYSNISRVAVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPA 180
QY 181 LRTTPSADHHVEAMVQMLHFRWNWIIIVLSSDITYGRDNGQLLGERVARRDICIAFOETL 240
Db 181 LRTTPSADHHVEAMVQMLHFRWNWIIIVLSSDITYGRDNGQLLGERVARRDICIAFOETL 240
QY 241 PTLQPNQNMTEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLQNFTGAVWIA 300
Db 241 PTLQPNQNMTEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLQNFTGAVWIA 300
QY 301 SESWAIDPVLHNLTELGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db 301 SESWAIDPVLHNLTELGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECNCLNATLSFNTILRLSGERVVSVYSAVAVAHALHSLGCDKSTCTKRVPVWQL 420
Db 361 QECNCLNATLSFNTILRLSGERVVSVYSAVAVAHALHSLGCDKSTCTKRVPVWQL 420
QY 421 LEEIWKVNFTLLDHQIFDPQGDVALHLEIVQWQDRSQNPFSQSVASYYPQLQKNIQD 480
Db 421 LEEIWKVNFTLLDHQIFDPQGDVALHLEIVQWQDRSQNPFSQSVASYYPQLQKNIQD 480
QY 481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACP 540
Db 481 ISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACP 540
QY 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFMLMTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIARSFQIVCAF 660
Db 601 GPMCFMLMTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIARSFQIVCAF 660
QY 661 MASRFPRAYSYVRYQGPVYVSMAPITVLKMVIVIGMLATGLSPTTRTDPDDPKITIVSC 720
Db 661 MASRFPRAYSYVRYQGPVYVSMAPITVLKMVIVIGMLATGLSPTTRTDPDDPKITIVSC 720
QY 721 NPNVRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFYFTSSVSLCTFM 780
Db 721 NPNVRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRD 839

RESULT 2
Q9Z0R7
ID Q9Z0R7 PRELIMINARY; PRT; 843 AA.
AC Q9Z0R7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative taste receptor TR2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=99159821; PubMed=10052456;
RA Hoon M.A., Adler E., Lindemeier J., Battey J.F., Ryba N.J.,
RA Zuker C.S.;
RT "Putative mammalian taste receptors: a class of taste-specific GPCRs
RT with distinct topographic selectivity."
RL Cell 96:541-551(1999).
DR EMBL; AF127390; AAD18070.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 2.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER 843
SQ SEQUENCE 843 AA; 95799 MW; D23AC22D21E049B8 CRC64;

Query Match 72.7%; Score 3231; DB 2; Length 843;
Best Local Similarity 70.8%; Pred. No. 3.3e-231;
Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFFLLWVLAEP--AENSDFYLPDGYLLGGLFSLHANMKGIHNLFLQVP 57
Db 1 MGPRARTCLLSLLHLVLPKPKLVENSDFHLAGDYLLGGLFTLHANVKSISHLSYLQVP 60

QY 58 MCKEYEVKIVGNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCYISNNQPVLYFLAH 117
Db 61 KCNEFTMKVLGYNLMQAMRFAVEEINNCSLLPGVLLGYEMVDVCYLSNNIHPGLYFLAQ 120

QY 118 EDNLLPIQEDYSNISRVAVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVR 177
Db 121 DDDLLPILKDYQYMPHVAVIGPDNSESATVSNILSHFLIPQITYSAISDKLRDRHF 180

QY 178 PALLRTTPSADHHVEAMVQMLHFRWNWIIIVLSSDITYGRDNGQLLGERVAR-RDICI 236
Db 181 PSMLRTVPSATHHIEAMVQMLVHFQWNWIIIVLSSDITYGRDNGQLLGERVAR-RDICI 240

QY 237 QETLPTLQPNQNMTEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLQNFTGA 296
Db 241 QEVLPPESSQVMRSEQRQDNLDKLRRTSARVVVVFSPDLTYHFFNEVLQNFTGF 300

QY 297 VWIASESWAIDPVLHNLTELGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQS 356
Db 301 VWIASESWAIDPVLHNLTELGTFLGTIVQSVIPGFSQFVRVRDKPGYPVNTNLR 360

QY 357 YTCNQECNCLNATLSFNTILRLSGERVVSVYSAVAVAHALHSLGCDKSTCTKRVPV 416
Db 361 TTCNQDCDACLNTTKSFNNILILSGERVVSVYSAVAVAHALHRLGNCNRVRCRKQKV 420

QY 417 PWQLLEIWKVNFTLLDHQIFDPQGDVALHLEIVQWQDRSQNPFSQSVASYYPQLQK 476
Db 421 PWQLLEIWKVNFTLLGNLFFDQGDMPMLDIIQWQDLNQNPFSQSVASYPSKRLT 480

QY 477 NIQDISWHTVNNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQ 536
Db 481 YINNVSWYTPNNTVPVSMCKSCQPGQMKKSVGLHPCCFECIDCMPTGTYLNRSADEF 540

QY 537 ACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTP 596
Db 541 SCPGSWWSYKNDITCFQRRPTFLEWHEVPTIVVAILAALGFFSTLAILVIFWRHFQ 600

QY 597 RSAGGPMCFMLMTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIARSF 656
Db 601 RSAGGPMCFMLMTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIARSF 660

QY 657 CAFKMASRFPRAYSYVRYQGPVYVSMAPITVLKMVIVIGMLATGLSPTTRTDPDDPK 716
Db 661 CVFKMARLPSAYSFWMRVHGPYVFAFITAKVALVGNMLATTINPIGRTPDDPNIM 720

QY 717 IVSCNPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFYFTSSV 776
Db 721 ILSCHPNYRNSLLFNTSLDLLSVVGFSPAYMGKELPTNYNEAKFTLSMTFYFTSS 780

QY 777 CTFMSAYSGLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGY 836
Db 781 CTFMSVHDGVLVTIMDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGY 840

QY 837 RR 838
Db 841 RK 842

RESULT 3
Q92514 ID Q92514 PRELIMINARY; PRT; 843 AA.
AC Q92514;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Candidate taste receptor T1r2.
GN Name=Tas1r2; Synonyms=T1r2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21219400; PubMed=11319557;
RA Montmayeur J.P., Liberles S.D., Matsunami H., Buck L.B.;
RT "A candidate taste receptor gene near a sweet taste locus.";
RL Nat. Neurosci. 4:492-498 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Montmayeur J.-P., Liberles S.D., Matsunami H., Buck L.B.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337041; AAK39438.1; -.
DR MGD; MGI:1933546; Tas1r2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 2.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 843 AA; 95735 MW; 0543834EA4E7AC2E CRC64;

Query Match 71.8%; Score 3191; DB 2; Length 843;
Best Local Similarity 69.4%; Pred. No. 3.le-228;
Matches 584; Conservative 113; Mismatches 141; Indels 4; Gaps 2;

QY 1 MGPRAKTICSLFFLLMVLAEP--AENSDFYLPDGYLLGGLFSLHANMKGIVHNLQVP 57
Db 1 MGPOARTLHLLFLLHALPKPVMVLVGNDSDFHLAGDYLGLFTLHANVKSVSLSYLQVP 60
QY 58 MCKEYEVKVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQVLYFLAH 117
Db 61 KCNEYNMKVLGYNLMQAMRFAVEEINNCSSLLPGVLLGYEMVDVCYLSNNIQPLGLYFLSQ 120
QY 118 EDNLLPIQEDYSNYSRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKRVRF 177
Db 121 IDDFLPILKDYQYRPQVAVIGPDNSESATVSNILSYFLVPQVITYSAITDKLRDKRRF 180
QY 178 PALLRTTPSADHHEAMVQMLHFRWNWIIVLSSDITYGRDNGQLLGERVARR-DICIAF 236
Db 181 PAMLRTVPSATHHIEAMVQMLVHFQNNWIVLVSDDDYGRNSHLLSQRLLTNGDICIAC 240
QY 237 QETLPTLPQNQNMSTSEERQRLVTIVDKLQQSTARVVVVFSPDLTYHFFNEVLQNFIGA 296
Db 241 QEVLPVPEPNQAVRPEQQLDNLDKLRRTSARVVVIFSPELSLHNFREVLWNFTGF 300
QY 297 VWIASESWAIDPVLHNLTELGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQS 356
Db 301 VWIASESWAIDPVLHNLTELHRTGTFLGLVTIQRVSIPIGFSQFRVRHDKPEYMPNETSLR 360

QY 357 YTCNQECNCLNATLSFNTILRSGERVVYVSAYAVAHALHSLGCDKSTCTKRVVY 416
Db 361 TTCNQCDACMNITESFNNVLMLSGERVVYVSAYAVAHALHSLGCDKSTCTKRVVY 420
QY 417 PWQLLEEIKVNFNTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPQSVASYYPLQRLK 476
Db 421 PWQLLREIWHVNFNTLLGNQLFFDEQDMPMLLDIIQWQGLSQNPQSVASYYPTETRLT 480
QY 477 NIQDISWHTVNTTIPMSMCKSCQSQKQKPKVGIHVCCFECIDCLPGTFLNHTDEYECQ 536
Db 481 YISNVSWYTPNTVPISMCKSKSCQKQKPKIPLHPCCFECVDCPPGTYLNRSDFNCL 540
QY 537 ACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFSTLAILVIFWRHFQTPIV 596
Db 541 SCPGSMWSYKNNIACFKRRRLAFLEWHEVPTIVVTILAAALGFSTLAILVIFWRHFQTPMV 600
QY 597 RSAGGPMCFMLTLLVAYVMVYVVGPPKVSTCLCRQALFPLCFTICISCIARSFQIV 656
Db 601 RSAGGPMCFMLVPLLLAFGMVYVVGPPKTVFSCFRCQAFFTVCFVCLSCITVRSFQIV 660
QY 657 CAFKMASRFPRAYSWYVYQGYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKIT 716
Db 661 CVFKMARRLPSAYGFWMRXHGYPVFAFITAVKVALVAGNMLATTINPIGRTPDDPNII 720
QY 717 IVSCNPYRNSLLFNTSLDILLVSVGFSGFAYMGKELPTNVNEAKFITLSMTFYFTSSVSL 776
Db 721 ILSCHPNYRNGLLFNTSMDLLSVLGFSAFYVGKELPTNVNEAKFITLSMTFSTSSISL 780
QY 777 CTFMSAYSGVLTVIVDLVTLVNLALSLGFGPKCYMILFYPERNTPAYFNSMIQGYTM 836
Db 781 CTFMSVHDGVLVTIMDLVTLVNLFLAIGLGYFGPKCYMILFYPERNTSAYFNSMIQGYTM 840
QY 837 RR 838
Db 841 RK 842

RESULT 4
Q923J8 ID Q923J8 PRELIMINARY; PRT; 843 AA.
AC Q923J8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sweet taste receptor T1r2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21400448; PubMed=11509186;
RA Nelson G., Hoon M.A., Chandrashekar J., Zhang Y., Ryba N.J.P.,
RA Zuker C.S.;
RT "Mammalian sweet taste receptors.";
RL Cell 106:381-390 (2001).
DR EMBL; AY032623; AAK51604.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 2.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 843 AA; 95752 MW; FD3C6B9B23270DA3 CRC64;

Query Match 71.6%; Score 3179; DB 2; Length 843;

Best Local Similarity 69.1%; Pred. No. 2.4e-227;		Matches 582; Conservative 114; Mismatches 142; Indels 4; Gaps 2;	
QY	1	MGPRAKTICSLFFLLWVLAEP---AENSDFYLPDGYLLGGLFSLHANMKGIHVLNQLQVP	57
Db	1	MGPOARTLHLLFLLHALPKPVMVLVGNDSFHLGAGLYLLGGLFTLHANVKSIVSHLSYLQVP	60
QY	58	MCKEYEVKIVGYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVVCIYISNNVQPVLYFLAH	117
Db	61	KCNEYNMKVLGYNLMQAMRFAVEEINNCSLLPGVLLGYEMVDVVCYLSNNIQPLGFLSQ	120
QY	118	EDNLLPIQEDYSNIYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKRVRF	177
Db	121	IDDFLPILKDYQYRPPQVAVIGPDNSESATVSNILSYFLVPQVTYSAITDKLQKRRF	180
QY	178	PALLRTTPSADHHVAMVQMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARR-DICIAF	236
Db	181	PAMLRTVPSATHHIEAMVQMLMHFQWNWIVLVSDDDYGRNSHLLSQRLTNTGDICIAF	240
QY	237	QETLPTLQPNQNMTEERQRLVTIVDKLQQSTARVVVVFSPDLTYHFFNEVLNQFTGA	296
Db	241	QEVLPVPEPNQAVRPEEQDQLDNILDKLRRTSARVVVIFSPELSLHNFREVLRWNFTGF	300
QY	297	VNIASESWAIDPVLHNLTELGHGTFLGITIQSVPIPGFSEFEWGPQAGPPPLSRTSQS	356
Db	301	VNIASESWAIDPVLHNLTELHRTGTFLGVTIQRSIPGFSQFRVRHDKPGYRMPNETSLR	360
QY	357	YTCNQCDCNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVVY	416
Db	361	TTCNQDCDACMNITESFNVLMLSGERVVYSVAVYVAHTLHLLHCNQVRCIKQIVY	420
QY	417	PWQLLEIWKVNFLLDHOIFFDPQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLK	476
Db	421	PWQLLEIWHVNFLLGNQLFFDEQDMPMLDDIIQWQGLSQNPFSQSVASYPTETRLT	480
QY	477	NIQDISWHTVNTNIPMSMCKRQSQGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQ	536
Db	481	YISNVSWYTPNNTVPISMCKSKCQPGQMKKPIGLHPCCFECVDCPDPTYLNRSDFNCL	540
QY	537	ACPNNWSYQSETSCFKRQLVFLWHEAPTIALLAALGFLSTLAILVIFWRHFQTPIV	596
Db	541	SCPGSMWSYKNNIACFKRLAFLWEHEVPTIVVTILAAFGFISTLAILLIFWRHFQTPMV	600
QY	597	RSAGGPMCFMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISIAVRSQIV	656
Db	601	RSAGGPMCFMLVPLLLAFGMVVPVYVGPVFCFCRQAFVFCVSVCLSCITVRSQIV	660
QY	657	CAFKMASRFPFRAYSVMRYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPDDPKIT	716
Db	661	CVFKMARRLPISAYGFWRYHGPYVFAFITAVKVALVAGNMLATTINPIGRTPDDPNII	720
QY	717	IVSCNPNYRNSLLENTSLDLLSVVGFSAFMGKELPTNYNEAKFITLSMTFFYFTSSVSL	776
Db	721	ILSCHPNYRNGLENTSMDLLSVLGFSAFMGKELPTNYNEAKFITLSMTFFSFTSSISL	780
QY	777	CTFMSAYSGLVVTIVDILLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNMIQGYTM	836
Db	781	CTFMSVHDGVLVTINDLLVTVLNFLAIGLGYFGPKCYMILFYPERNTSAYFNMIQGYTM	840
QY	837	RR 838	
Db	841	RK 842	

RESULT 5
Q7TP27
ID Q7TP27 PRELIMINARY; PRT; 1465 AA.
AC Q7TP27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bal-651.
OS Rattus norvegicus (Rat).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Xu C.S., Li W.Q., Li Y.C., Wang L., Wang S.F., Han H.P., Wang G.P.,
RA	Chai L.Q., Yuan J.Y., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
RA	Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY325227; AAP92628.1; -
DR	GO; GO:0005759; C:mitochondrial matrix; IEA.
DR	GO; GO:0003842; F:1-pyrroline-5-carboxylate dehydrogenase act. . .; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0008152; P:metabolism; IEA.
DR	GO; GO:0006561; P:proline biosynthesis; IEA.
DR	InterPro; IPR002086; Aldehyde_dehydr.
DR	InterPro; IPR001828; ANF_receptor.
DR	InterPro; IPR005931; DlpYr5carbox1.
DR	Pfam; PF00171; Aldedh; 1.
DR	Pfam; PF01094; ANF_receptor; 1.
DR	TIGRFAMS; TIGR01236; DlpYr5carbox1; 1.
DR	PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR	PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
SQ	SEQUENCE 1465 AA; 163958 MW; E50B012FFDBF84EB CRC64;
	Query Match 39.2%; Score 1741; DB 2; Length 1465;
	Best Local Similarity 61.4%; Pred. No. 4.1e-120;
	Matches 336; Conservative 69; Mismatches 84; Indels 58; Gaps 3;
QY	1 MGPRAKTICSLFFLLWVLAEP---AENSDFYLPDGYLLGGLFSLHANMKGIVHLNQLQVP 57
Db	896 MGPOARTLCLLSLLHVLVLPKPKLVENSDFHLGAGLYLLGGLFTLHANVKSISHLSYLQVP 955
QY	58 MCKE-----YE 63
Db	956 KCNDNVGDDGGGADVIVVGDHKKHMTVMVAVLVGWDMPVTAGMAVMEVTVGVNGQWFT 1015
QY	64 VKVIGYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVVCIYISNNVQPVLYFLAHEDNLLP 123
Db	1016 MKVLGYNLMQAMRFAVEEINNCSLLPGVLLGYEMVDVVCYLSNNIHPGLYFLAQDDDLLP 1075
QY	124 IQEDYSNIYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKRVFPALLRT 183
Db	1076 ILKDYSQYMPHVAVIGPDNSESATVSNILSHFLIPQITYSAISDKLRDKRHFPSMLRT 1135
QY	184 TPSADHHVAMVQMLHFRWNWIIVLVSSDTYGRDNGQLLGERVAR-RDICIATQETLPT 242
Db	1136 VPSATHHIEAMVQMLMHFQWNWIVLVSDDDYGRNSHLLSQRLTKTSDICIAFQEVLP 1195
QY	243 LOPNQNMTESEERQRLVTIVDKLQQSTARVVVVFSPDLTYHFFNEVLNQFTGAVWIASE 302
Db	1196 PESSQVMSRSEERQRLDNILDKLRRTSARVVVVFSPPELSLSYFFHEVLWNFTGFVWIASE 1255
QY	303 SWAIDPVLHNLTELGHGTFLGITIQSVPIPGFSEFEWGPQAGPPPLSRTSQSYTCNQE 362
Db	1256 SWAIDPVLHNLTELHRTGTFLGVTIQRSVPIGFSQFRVRDRKPGYPVENTNLRITTCNQD 1315
QY	363 CDNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVVYPWQLLE 422
Db	1316 CDACLNTTKSFNNILILSGERVVYSVAVYVAHALHRLGCRNRVRCCTKQKVPWQLLR 1375
QY	423 EIKVNFLLDHOIFFDPQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLKNIQDIS 482
Db	1376 EIWHVNFLLGNRLFFDQGDMPMLDDIIQWQDLSQNPFSQSVASYPSKRLTYINNVS 1435
QY	483 WHTVNTT 489
Db	1436 WYTPNNT 1442

RESULT 6
Q9Z0R8
ID Q9Z0R8 PRELIMINARY; PRT; 840 AA.


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QY 27 FYLPDGYLLGGLFSLHANMKGIVHLNLFLOVPMC-KEYEVKVIQYNLMQAMRFAVEEINND 85
Db 33 FSLPGDFLLAGLFSLHADCLQVRHRPL--VTSCDRSDSFNGHGYHLFQAMRFTVEEINNS 90
QY 86 SSSLPGVLLGYEIVDVCYISNNVQPVLYFLAHE-DNLLPIQEDYSNIYSRVVAVIGPDNS 144
Db 91 TALLPNITLGYELYDVCSESSNVYATLRVLAQQGTGHEMQRDLRNHSSKVVALIGPDNT 150
QY 145 ESVMTVANFLSLFLLPQITYSAISDELDRKVRFPALLRTPSADHHVEAMVQMLHFRWN 204
Db 151 DHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPFLRTIPSDKYQVEVIVRLQSGFVW 210
QY 205 WIIVLVSSDTYGRDNGQLLGERVARRDICIATFQETLPTLQPNQNMNTSEERQRLVTIVDKL 264
Db 211 WISLVGSYGDYQGLGVQALEELATPRGICVAFKDVVPL---SAQAGDPRMQRMML---RL 264
QY 265 QQSTARVVVVFSPDLTLYHFFNEVLNQFTGAVWIASWAIIDPVLHNLTELGHGLGFLG 324
Db 265 ARARTVVVVFNRHLGAVFFRSVVLANLTGKVIASEDWAISTYITNVPGIQIGITVLG 324
QY 325 ITIQSVPIPGFSEFREWGPQA--GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE 382
Db 325 VAIQORQVPGGLKEFEESYVQAVTGAPRTCPGSGWCCTNQLCRECHAFITWNMPGLGAFSM 384
QY 383 RVVYSVYSAYAVAHALHSLGCDKSTCTKRVPVYPWQLLEIWKVNFLLDQIIFDPOG 442
Db 385 SAAYNVYEAVYAVAHGLHQLLGTSGTCARGPVYPWQLLQOIYKVNFLHKKTVAFDDXG 444
QY 443 DVALHLEIVQWQDRSQNPFSQV--ASYYPQLORQLKNIQDISWHTVNTTIPMSMCKRCQ 500
Db 445 DPLGYDIIAWDNGPEWTFEIVGSASLSPVHLDI-NKTKIQWHGKNNQVPVSVCTRDCL 503
QY 501 SGQKKPVGIVHCCFECIDCLPGTFNLNHTEDYEYECQACPNNEWSYQSETSCFKRQLVFL 560
Db 504 EGHRLVMGSHHCCFECMPCGAGTFLN-TSELHTCQPCGTGTEWAPGESSACFSRTVEFLG 562
QY 561 WHEAPTIALLAALGFLSTLAILVIF-----WRHFQTPIVRSAGGPMCFMLTLLV 613
Db 563 WHE--PISLVLLAA---NTLLLLLLIGTAGLFAWR-LHTPVVRSAGGRLCFLMLGSLVA 615
QY 614 AYVVVYVYVPPKSTCLCRQALFPLCFTICISCIARSFOIVCAFKMASRFPRAYSYVW 673
Db 616 GSCSLYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIFKFSTKVPTFYHTWA 675
QY 674 RYQGPVYSMAFITVLKMV--IVVIGMLATGLSPTRTDPDDPKITIVSCNPNYRNSLLEN 731
Db 676 QNHGAGI---FVIVSSTVHLFCLTLWAMWTPRPTREYQRFPHLVILECTEVNSVGFLVA 732
QY 732 TSLDLLLLSVVGFSAFYMKGELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGLVLTIV 791
Db 733 FAHNILLISITFVCSYLGKELPENYNEAKCVTFSLLLHFFVSWIAFTMSSIIYQGSYLPV 792
QY 792 DLLVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837
Db 793 NVLAGLATLSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRR 838
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RESULT 8
Q99PG5
ID Q99PG5 PRELIMINARY; PRT; 842 AA.
AC Q99PG5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative sweet taste receptor Tlrl (Fragment).
GN Name=Taslrl; Synonyms=Gpr70;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```
RC STRAIN=129P3/J;  
RX MEDLINE=21030739; PubMed=11178737;  
RA Li X., Inoue M., Reed D.R., Huque T., Puchalski R.B., Tordoff M.G.,  
RA Ninomiya Y., Beauchamp G.K., Bachmanov A.A.;  
RT "High-resolution genetic mapping of the saccharin preference locus  
RT (Sac) and the putative sweet taste receptor (Tlrl) gene (Gpr70) to  
RT mouse distal Chromosome 4.";  
RL Mamm. Genome 12:13-16(2001).  
DR EMBL; AF301162; AAK07092.1; --  
DR HSSP; P23385; IEWK.  
DR MGD; MGI:1927505; Taslrl.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001828; ANF_receptor.  
DR InterPro; IPR000068; Ca_sens_receptor.  
DR InterPro; IPR000345; Cytc_heme_BS.  
DR InterPro; IPR000337; GPCR_Mgr.  
DR InterPro; IPR011500; NCD3G_GPCR.  
DR Pfam; PF00003; 7tm_3; 1.  
DR Pfam; PF01094; ANF_receptor; 1.  
DR Pfam; PF07562; NCD3G; 1.  
DR PRINTS; PR00592; CASENSINGR.  
DR PRINTS; PR00248; GPCR_MGR.  
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.  
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.  
KW Receptor.  
FT NON_TER 842 842  
SQ SEQUENCE 842 AA; 93428 MW; 39739A2FF482D33F CRC64;
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Query Match 32.6%; Score 1446.5; DB 2; Length 842;  
Best Local Similarity 40.0%; Pred. No. 1.6e-98;  
Matches 330; Conservative 120; Mismatches 341; Indels 35; Gaps 15;  
QY 27 FYLPDGYLLGGLFSLHANMKGIVHLNLFLOVPMC-KEYEVKVIQYNLMQAMRFAVEEINND 85  
Db 33 FSLPGDFLLAGLFSLHADCLQVRHRPL--VTSCDRSDSFNGHGYHLFQAMRFTVEEINNS 90  
QY 86 SSSLPGVLLGYEIVDVCYISNNVQPVLYFLAHE-DNLLPIQEDYSNIYSRVVAVIGPDNS 144  
Db 91 TALLPNITLGYELYDVCSESSNVYATLRVLAQQGTGHEMQRDLRNHSSKVVALIGPDNT 150  
QY 145 ESVMTVANFLSLFLLPQITYSAISDELDRKVRFPALLRTPSADHHVEAMVQMLHFRWN 204  
Db 151 DHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPFLRTIPSDKYQVEVIVRLQSGFVW 210  
QY 205 WIIVLVSSDTYGRDNGQLLGERVARRDICIATFQETLPTLQPNQNMNTSEERQRLVTIVDKL 264  
Db 211 WISLVGSYGDYQGLGVQALEELATPRGICVAFKDVVPL---SAQAGDPRMQRMML---RL 264  
QY 265 QQSTARVVVVFSPDLTLYHFFNEVLNQFTGAVWIASWAIIDPVLHNLTELGHGLGFLG 324  
Db 265 ARARTVVVVFNRHLGAVFFRSVVLANLTGKVIASEDWAISTYITNVPGIQIGITVLG 324  
QY 325 ITIQSVPIPGFSEFREWGPQA--GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE 382  
Db 325 VAIQORQVPGGLKEFEESYVQAVTGAPRTCPGSGWCCTNQLCRECHAFITWNMPGLGAFSM 384  
QY 383 RVVYSVYSAYAVAHALHSLGCDKSTCTKRVPVYPWQLLEIWKVNFLLDQIIFDPOG 442  
Db 385 SAAYNVYEAVYAVAHGLHQLLGTSGTCARGPVYPWQLLQOIYKVNFLHKKTVAFDDNG 444  
QY 443 DVALHLEIVQWQDRSQNPFSQV--ASYYPQLORQLKNIQDISWHTVNTTIPMSMCKRCQ 500  
Db 445 DPLGYDIIAWDNGPEWTFEIVGSASLSPVHLDI-NKTKIQWHGKNNQVPVSVCTRDCL 503  
QY 501 SGQKKPVGIVHCCFECIDCLPGTFNLNHTEDYEYECQACPNNEWSYQSETSCFKRQLVFL 560  
Db 504 EGHRLVMGSHHCCFECMPCGAGTFLN-TSELHTCQPCGTGTEWAPGESSACFSRTVEFLG 562  
QY 561 WHEAPTIALLAALGFLSTLAILVIF-----WRHFQTPIVRSAGGPMCFMLTLLV 613  
Db 563 WHE--PISLVLLAA---NTLLLLLLIGTAGLFAWR-LHTPVVRSAGGRLCFLMLGSLVA 615  
QY 614 AYVVVYVYVPPKSTCLCRQALFPLCFTICISCIARSFOIVCAFKMASRFPRAYSYVW 673  
Db 616 GSCSLYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIFKFSTKVPTFYHTWA 675  
QY 674 RYQGPVYSMAFITVLKMV--IVVIGMLATGLSPTRTDPDDPKITIVSCNPNYRNSLLEN 731  
Db 676 QNHGAGI---FVIVSSTVHLFCLTLWAMWTPRPTREYQRFPHLVILECTEVNSVGFLVA 732  
QY 732 TSLDLLLLSVVGFSAFYMKGELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGLVLTIV 791  
Db 733 FAHNILLISITFVCSYLGKELPENYNEAKCVTFSLLLHFFVSWIAFTMSSIIYQGSYLPV 792  
QY 792 DLLVTVLNLALISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837  
Db 793 NVLAGLATLSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRR 838
```

QY 614 AYMVVYVVGPPKYSTCLCRQALFPLCFTICISCIARSFQIVCAFKMARSFPRAYSIVV 673

Db 616 GSCSLYSFFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIKFSTKVTFYHTWA 675

QY 674 RYQGPVYSMAFITVLKMW--IVVIGMLATGLSPTRTDDPKITIVSCNPNYRNSLLFN 731

Db 676 QNHGAGI---FVIVSSTVHLFLCLTLWLMWTPRPTREYQRFPHLVILECTEVNSVGFLVA 732

QY 732 TSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGLVLTIV 791

Db 733 FAHNILLSISTFVCSYLKELPENYNEAKCVTFSLLLHFVSWIAFFTMSIIYQGSYLPV 792

QY 792 DLLVTVNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837

Db 793 NVLAGLATLGGFGYFLPKCYVILCRPELNNTHEHFQASIQDYTRR 838

RESULT 9

Q923J9 PRELIMINARY; PRT; 842 AA.

AC Q923J9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Taste receptor Tlr1.

GN Name=Tas1r1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21400448; PubMed=11509186;

RA Nelson G., Hoon M.A., Chandrashekar J., Zhang Y., Ryba N.J.P., Zuker C.S.;

RT "Mammalian sweet taste receptors.";

RL Cell 106:381-390(2001).

DR EMBL; AY032622; AAK51603.1; -.

DR HSSP; P23385; IEWK.

DR MGD; MGI:1927505; Tas1r1.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR001828; ANF receptor.

DR InterPro; IPR000068; Ca_sens_receptor.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR000337; GPCR_Mgr.

DR InterPro; IPR011500; NCD3G_GPCR.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR Pfam; PF07562; NCD3G; 1.

DR PRINTS; PR00592; CASENSINGR.

DR PRINTS; PR00248; GPCRMRGR.

DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.

DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.

KW Receptor.

SQ SEQUENCE 842 AA; 93455 MW; D4D2CE90959E991A CRC64;

Query Match 32.4%; Score 1440.5; DB 2; Length 842;

Best local Similarity 39.8%; Pred. No. 4.3e-98;

Matches 329; Conservative 121; Mismatches 341; Indels 35; Gaps 15;

QY 27 FYLPGDYLLGGFLSHANMKGIVHLNLFQVPMC-KEYEVKVIQYNLMQAMRFAVEEINND 85

Db 33 FSLPGDFLLAGFLSHADCLQVRRPL--VTSCDRSDSFNGHYHLFQAMRFTVEEINNS 90

QY 86 SSLLPGVLLGYEIVDVVCYISNNVQPVLYFLAHE-DNLLPIQEDYSNYISRVVAVIGPDNS 144

Db 91 TALLPNITLGYELYDVCSSESNVYATLRVPAQQTGHLEMQRDLRNHSSKVVALIGPDNT 150

QY 145 ESMVTVANFLSLFLPQITYSAISDELDRDKVRFPALRTTPSADHHVEAMVQLMHLFRWN 204

Db 151 DHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPFLRTIPSDKYQVEVIVRLQSFQWV 210

QY 205 WIIVLVSSDTYGRDNGQLLGERVARRDICIARFQETLPTLPNQNMNTSEERQRLVTIVDKL 264

Db 211 WISLVGSYGDYQGLGVQALEELATPRGICVAFKDVVPL---SAQAGDPRMQRMML---RL 264

QY 265 QQSTARVVVVFSPDLTLHYHFFNEVLQRNFTGAVWIASWAIADPVLHNLTELCHLGTFLG 324

Db 265 ARARTVVVVFSPNHLAGVFRSVVLANTLGKWKVIASEDWAISTYITNVPGIQTIVLG 324

QY 325 ITIQSVPIPGSEFREWGPQA--GPPPLSRTSQSYTCNQECDNCLNATLSNTILRLSGE 382

Db 325 VAIQORQVPGLEFEESYVQAVMGAPRTCPEGSWCGTNQLCRECHAFTTWNMPELGAFSM 384

QY 383 RVVYSVYSAVAVAHALHSLGCDKSTCTKRVVYPWQLLEEIKWKNFTLLDHQIFFDPQG 442

Db 385 SAAYNVYEAVAVAHGLHQLLGLCTSGTCARGPVYPWQLLQIYKVNFLHKKTVAFDDKG 444

QY 443 DVALHLEIVQWQDRSQNPFSV--ASYYPLOQLKNIQDISWHTVNNTIMSGMSKRCQ 500

Db 445 DPLGYDIIANDWNGPEWTFEIGSASLSPVHLDI-NKTKIQWHGKNNQVPVSVCTRDCL 503

QY 501 SGQKKKPVGIHVCCECIDCLPGTFLNHTDEYECQACPNNEWYSQSETSCPKRQLVFL 560

Db 504 EGHRLVMGSHHCCFECMPCEAGTFLN-TSELHTCQPCGTEEWAPEGSSACFSRTVEFLG 562

QY 561 WHEAPTIAVALLAALGFLSTLAILVIF-----WRHFQTPIVRSAGGPMCFMLTLTLLV 613

Db 563 WHE--PISLVLLAA---NTLLLLLLIGTAGLFAWR-LHTPVVRSAGGRLCFMLGSLVA 615

QY 614 AYMVVYVVGPPKYSTCLCRQALFPLCFTICISCIARSFQIVCAFKMARSFPRAYSIVV 673

Db 616 GSCSLYSFFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIKFSTKVTFYHTWA 675

QY 674 RYQGPVYSMAFITVLKMW--IVVIGMLATGLSPTRTDDPKITIVSCNPNYRNSLLFN 731

Db 676 QNHGAGI---FVIVSSTVHLFLCLTLWLMWTPRPTREYQRFPHLVILECTEVNSVGFLVA 732

QY 732 TSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGLVLTIV 791

Db 733 FAHNILLSISTFVCSYLKELPENYNEAKCVTFSLLLHFVSWIAFFTMSIIYQGSYLPV 792

QY 792 DLLVTVNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837

Db 793 NVLAGLATLGGFGYFLPKCYVILCRPELNNTHEHFQASIQDYTRR 838

RESULT 10

Q99PG6 PRELIMINARY; PRT; 842 AA.

AC Q99PG6;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative sweet taste receptor Tlr1 (fragment).

GN Name=Tas1r1; Synonyms=Gpr70;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6ByJ; PubMed=11178737;

RX MEDLINE=21030739;

RA Li X., Inoue M., Reed D.R., Huque T., Puchalski R.B., Tordoff M.G., Ninomiya Y., Beauchamp G.K., Bachmanov A.A.;

RT "High-resolution genetic mapping of the saccharin preference locus (Sac) and the putative sweet taste receptor (Tlr1) gene (Gpr70) to mouse distal Chromosome 4.";

RL Mamm. Genome 12:13-16(2001).

DR EMBL; AF301161; AAK07091.1; -.

DR HSSP; P23385; IEWK.

DR MGD; MGI:1927505; Tas1r1.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21888635; PubMed=11891061;
RA Makalowska I., Sood R., Faruque M.U., Hu P., Robbins C.M.,
RA Edgings E.M., Mestre J.D., Baxevanis A.D., Carpten J.D.;
RT "Identification of six novel genes by experimental validation of
RT GeneMachine predicted genes.";
RL Gene 284:203-213 (2002).
DR EMBL; AF387618; AAL91359.1; -.
DR HSSP; P23385; 1ISS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 763 AA; 84427 MW; 593616575D6BD17D CRC64;

Query Match 28.2%; Score 1251; DB 2; Length 763;
Best Local Similarity 37.0%; Pred. No. 4.7e-84;
Matches 288; Conservative 124; Mismatches 331; Indels 36; Gaps 13;

QY 75 MRFAVEEINNDSSLLPGVLLGVEIVDVVCYISNNVQPVLYFLA----HEDNLLPIQEDYSN 130
DB 1 MRLGVEEINNSTALLPNITLGQLYDVCDSDSANVYATLRVLSLPGQHH---IELQGLLH 57

QY 131 YISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKVRFPALLRRTTFSADHH 190
DB 58 YSPITLAVIGPDSTNRAATTAALLSPFLVPMISYAASSETLSVKRQPSFLRTIPNDKYQ 117

QY 191 VEAMVQLMLHFRWNWIIVLSSDPTGRDNGQLLGERVARRDICIATFQETLP-TLQPNQNM 249
DB 118 VETWVLLQKFGWTWISLVGSSDYGQLGVQALENAQTGQICIAFKDIMPFSAQVGD-- 175

QY 250 TSEERQRLVTIVDKLQOSTARVVVVFSPDLTLHYHFEVNLKQNTGAVWIASESWAIDPV 309
DB 176 -----ERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLNLTGKVVVASEAWLSRH 230

QY 310 LHNLTGLHGLTFLGITIQSVPIPGFSEFREWGPQA---GPPLSRTSQSYTCNQECNDC 366
DB 231 ITGVPGIQRIGMVLGVAIQRAVPGPKAFEEAYARADKXAPRPHKGSWC-SSNQLCREC 289

QY 367 LNATLSFNTILRLSGERVVSVYSAYAVAHALHSLGCDKSTCTKRVVVPWQLLEEIKW 426
DB 290 QAFMAHTMPKLFKAFSMSSAYNAYRAVYAVAHGLHQLLGCASGACSRGRVYPWQLLEQIHK 349

QY 427 VNTLLDHIQIFDPQGDVALHLEIVQWQWDRSQNPFSQVAS--YYPQLRQLKNIQDISWH 484
DB 350 VHFLLHKDTVAFNDNRDPLSSYNIIAWDWNWGPKWTFTVLGSSTWSPVQLNI-NETKIQWH 408

QY 485 TVNNTIPMSMCKRCQSQGQKKPVGIHVCCFECIDCLPGTFLNHTEDYEYECQACPNNEWS 544
DB 409 GKDNQVPKSVCSDDCLEGHQRVVTFGPHHCCFECVPCGAGTFLNKS-DLYRCQPCGKEWA 467

QY 545 YQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVFWRHFTQPIVRSAGGPMC 604
DB 468 PEGSQTCPFRTPVFLALREHTSWVLLAANTLILLLLGLTAGLFAWHLDTPVRSAGGRLC 527

QY 605 FLMLTLLLVAYMVVVPVGPVKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFKMASR 664
DB 528 FLMLGSLAAGSGSLYGFEXEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSK 587

QY 665 FPRAYSVWRYQGPYVSMAFITVLKMWIVVIGMLATGLSPTRTDDPDKITIVSCNPY 724

DB 588 VPTFYHAWQNHGAGLFWMISSAAQLLICLTWLVTWVPLP-AREYQRFPHLVMLECTET- 645
QY 725 RNSL-----LFNTSLDLLSVWGFSFAYMKGELPTNYNEAKFITLSMTFYFTSSVSLCT 778
DB 646 -NSLGFILAFLYNG---LLSISAFACSYLGKDLPENYNEAKCVTFSLLENFVSWIAFFT 700
QY 779 FMSAYSGVLVTTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMR 837
DB 701 TASVYDGKYLPAANNMAGLSSLSGFGGYFLPKCYVILCRPDNLNSTEHFQASIQDYTRR 759

RESULT 14
Q8JIO4
ID Q8JIO4 PRELIMINARY; PRT; 1027 AA.
AC Q8JIO4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium polyvalent cation receptor/salinity sensing protein.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hynostomalea; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22103704; PubMed=12093923;
RA Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,
RA Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;
RT "Polyvalent cation receptor proteins (CaRs) are salinity sensors in
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002).
DR EMBL; AF406649; AAM77700.1; -.
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;

Query Match 24.5%; Score 1089; DB 2; Length 1027;
Best Local Similarity 31.1%; Pred. No. 7.6e-72;
Matches 278; Conservative 161; Mismatches 360; Indels 96; Gaps 26;

QY 5 AKTICSLFFLLWVLAEPANSDYFLP-----GDYLLGGLFSLHANM--KGIVHLNPLQ 55
DB 2 AQLHCQLLFLGFTLLQ-SYNVSGYGNQRAQKGDIIILGLFPIHFVGAAKDQLKSRPE 60
QY 56 VPMCKEYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGVEIVDVC-YISNNVQPVLYF 114
DB 61 ATKIRYNFR--GFRWLQAMFAIEEINNMTFLPNITLGRIFDTCNTVSKALEATLSF 118
QY 115 LA-HEDNLLPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDEL 171
DB 119 VAQNKIDSLNDEFNCSDHPSTIAVVGATSGSIGISTAVANLLGLFYIPQVSYASSRLL 178
QY 172 RDKVRFPALLRTPPSADHHVEAMVQLMLHFRWNWIIVLSSDPTGRDNGQLLGERVARRD 231

Db 179 SNKNEYKAFRLTIPNDEQATAMAEIIIEHFQWNVVGTLLAADDYGRPGIDKFRBEAVKRD 238

QY 232 ICIAFQETLPTLPNQNMTESEERQRLVTIVDKLQOSTARVVVWFSPDLTLYHFFNEVLQR 291

Db 239 ICIDFSEMI-----SQYIT--QKQLEFIADVIQNSAKVIVFNSGPDLEPLIQEIVRR 290

QY 292 NFGAVWIASWAIQVPLHNLTELGHGLTFLGITIQSVPIPGFSEFRE----- 340

Db 291 NITDRIWLASEAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGENKFLKEVHPSRSSDNG 350

QY 341 -----W-----GPOA-GPPPLSRTSQSYTCNQECNCLNAT 370

Db 351 FVKEFWETFCYFTEKTLTQLKNSKVPSHGPAQQGDSKAGNSRRRTALRHPCTGEENIT 410

QY 371 LSFNTILRLSGERVVYSVAVYAVAHALHSLGCDKST-----CTK-RVVPWQLLE 422

Db 411 SVETPYLDYTHLRISYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLN 470

QY 423 EIWKVNFT-LLDHQIFFDPQGDVALHLEIVQWQDRSQNP--FQSVASY-----YPLQRQL 475

Db 471 HLHLKFTNSMGEQVDFDDQDLKGNYYTIINWQLSAEDESVLFEHVGYNAYAKPSDRLN 530

QY 476 KNIQDISWHTVNNITPMSCKSKRCQSQGKKPV-GIHVCCFECIDCLPGTFLNHTEDYE 534

Db 531 INEKKILWSGFSKVVPFNSCSRDCVPGTRKGIIEGPTCCFECMACAEGERF SDENDASA 589

QY 535 CQACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTP 594

Db 590 CTKCPNDFWSNENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTP 649

QY 595 IVRSAGGPMCFMLTLLLVAYMVVVPVVGPPKVVSTCLCRQALPPLCFTTICISIAVRSFQ 654

Db 650 IVKATNRELSYLLFLSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCIILVKTNR 709

QY 655 IVCAFKMASRFPRAYSVVRYQGPYVSMAFITVLKMWIIVWIGMLATGLSPTRTDPDDP 713

Db 710 VLLVFE--AKIPTSLHRKWVGLNLQFL-LVFLCILVQIVTCLIIWLYTAPPSSYRNHELED 766

QY 714 KITIVSCPNYRNSLIFNTSLDLLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFYFTSS 773

Db 767 EVIFITCDEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSLIEFIVM 826

QY 774 VS-LCTFMSAYSGVLVTIVDVLVTLNLLAISLGYFG-----PKCYMILFYPERNT 823

Db 827 ISFIPAYVSTY-GKFVSARE-----VIAILASSFGLGCIYFNKCYIILFKPCRN 876

RESULT 15

CASR_HUMAN STANDARD; PRT; 1078 AA.

AC P41180; Q13912; Q16108; Q16109; Q16110; Q16379;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).

DE Name=CASR; Synonyms=GPRC2A, PCAR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Pearce S.H.S., Thakker R.V.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Parathyroid;

RX MEDLINE=95279439; PubMed=7759551;

RA Garrett J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M.,

RA Hebert S.C., Nemeth E.F., Fuller F.;

RT "Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.";

RL J. Biol. Chem. 270:12919-12925(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=95408281; PubMed=7677761;

RA Aida K., Koishi S., Tawata M., Onaya T.;

RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from human kidney.";

RL Biochem. Biophys. Res. Commun. 214:524-529(1995).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=96343808; PubMed=8756555;

RA Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V.,

RA Raue F.;

RT "Expression of a calcium-sensing receptor in a human medullary thyroid carcinoma cell line and its contribution to calcitonin secretion.";

RL Endocrinology 137:3842-3848(1996).

RN [5]

RP SEQUENCE OF 643-908 FROM N.A.

RX MEDLINE=96193893; PubMed=8613532;

RA Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.;

RT "Changes in calcium responsiveness and handling during keratinocyte differentiation. Potential role of the calcium receptor.";

RL J. Clin. Invest. 97:1085-1093(1996).

RN [6]

RP VARIANTS FHH GLN-185; LYS-297 AND TRP-795.

RX MEDLINE=94094324; PubMed=7916660;

RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,

RA Steinmann B., Levi T., Seidman C.E., Seidman J.G.;

RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism.";

RL Cell 75:1297-1303(1993).

RN [7]

RP VARIANT ADH ALA-127.

RX MEDLINE=95179179; PubMed=7874174;

RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,

RA Hebert S.C., Seidman C.E., Seidman J.G.;

RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor gene mutation.";

RL Nat. Genet. 8:303-307(1994).

RN [8]

RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.

RX MEDLINE=95243222; PubMed=7726161;

RA Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist H.,

RA Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,

RA Seidman C.E.;

RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause familial hypocalciuric hypercalcemia.";

RL Am. J. Hum. Genet. 56:1075-1079(1995).

RN [9]

RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.

RX MEDLINE=95403641; PubMed=7673400;

RA Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;

RT "Familial hypocalciuric hypercalcemia associated with mutation in the human Ca(2+)-sensing receptor gene.";

RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).

RN [10]

RP VARIANTS NSHPT LEU-227 AND TYR-582.

RX MEDLINE=96292293; PubMed=8675635;

RA Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,

RA Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,

RA Thakker R.V.;

RT "Calcium-sensing receptor mutations in familial benign hypercalcemia and neonatal hyperparathyroidism.";

RL J. Clin. Invest. 96:2683-2692(1995).

RN [11]

RP VARIANTS FIH THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.

RX MEDLINE=96311554; PubMed=8733126;

RA Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L.,

RA Zimmerman D., Cutler G.B. Jr.;

RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal dominant and sporadic hypoparathyroidism.";

RL Hum. Mol. Genet. 5:601-606(1996).

RN [12]
RP VARIANT FHH ARG-174.
RX MEDLINE=97442275; PubMed=9298824;
RA Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
RA Ratajczak T.;
RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated
RT with familial hypocalcemic hypercalcemia.";
RL Hum. Mutat. 10:233-235(1997).
RN [13]
RP VARIANT FHH VAL-616.
RX MEDLINE=99415602; PubMed=10487661;
RA Stock J.L., Brown R.S., Baron J., Coderre J.A., Mancilla E.,
RA De Luca F., Ray K., Mericq M.V.;
RT "Autosomal dominant hypoparathyroidism associated with short stature
RT and premature osteoarthritis.";
RL J. Clin. Endocrinol. Metab. 84:3036-3040(1999).
RN [14]
RP VARIANT FHH GLU-557.
RX MEDLINE=21603857; PubMed=11762699;
RA Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aoi N.,
RA Kosuge K., Sato M., Ozawa Y., Kanmatsuse K., Kokubun S.;
RT "A novel mutation in Ca2+-sensing receptor gene in familial
RT hypocalcemic hypercalcemia.";
RL Endocrine 15:277-282(2001).
CC -!- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P41180-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P41180-2; Sequence=VSP 002035;
CC -!- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
CC liver, heart, skeletal muscle, or placenta.
CC -!- DISEASE: Defects in CASR are the cause of familial hypocalcemic
CC hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor
CC has reduced activity. FHH is characterized by altered calcium
CC homeostasis. Affected individuals exhibit mild or modest
CC hypercalcemia, relative hypocalciuria, and inappropriately normal
CC PTH levels.
CC -!- DISEASE: Defects in CASR are the cause of neonatal severe primary
CC hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor
CC has reduced activity. NSHPT is a rare autosomal recessive life-
CC threatening disorder characterized by very high serum calcium
CC concentrations, skeletal demineralization, and parathyroid
CC hyperplasia. In some instances NSHPT has been demonstrated to be
CC the homozygous form of FHH.
CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant
CC hypocalcemia (ADH) [MIM:601198]; in which the receptor is
CC activated at subnormal Ca(2+) levels.
CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant
CC hypoparathyroidism (FIH) [MIM:146200]. FIH is characterized by
CC hypocalcemia and hyperphosphatemia due to inadequate secretion of
CC parathyroid hormone. Symptoms are seizures, tetany and cramps.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X81086; CAA56990.1; -
CC EMBL; U20759; AAA86503.1; -
CC EMBL; U20760; AAA86504.1; -
CC EMBL; D50855; BAA09453.1; -
CC EMBL; S83176; AAB46873.1; -
CC EMBL; S79217; AAB35262.2; -

DR EMBL; S68032; AAB29413.2; ALT_SEQ.
DR EMBL; S68033; AAB29414.1; -
DR EMBL; S68036; AAB29415.1; -
DR EMBL; S81755; AAD14370.1; -
DR HSSP; P23385; 1EWK.
DR Genew; HGNC:1514; CASR.
DR MIM; 601199; -
DR MIM; 145980; -
DR MIM; 239200; -
DR MIM; 601198; -
DR MIM; 146200; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0005513; P:calcium ion sensing; TAS.
DR GO; GO:0007635; P:chemosensory behavior; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0001503; P:ossification; TAS.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
Query Match 24.3%; Score 1079.5; DB 1; Length 1078;
Best Local Similarity 31.4%; Pred. No. 4.1e-71;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;
QY 16 WVLAEPANSDFYLP-----GDYLLGGLFSLHANMKGIVHLNFLQVPMCKEYEVKVG 68
Db 8 WVLLALITWHTSAYGPDQRAQKKGDIILGGLFPIHF---GVAAKD--QDLKSRPESVECI 62
QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFRWLQAMIFAIEEINSSPALLPNLTGLGYRIFTCNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRPPA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATSGVSTAVANLGLFYIPQVSYASSRLLSNKNQFKS 182
QY 180 LLRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICI AFQET 239
Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGIIAADDYGRPGIEKFREEAEERDICI DFSEL 242
QY 240 LPTLPQNQNTSEERQLVTIIVDKLQQSTARVVVVFSPDLTLYHFFNEVLNQFTGAVMI 299
Db 243 I-----SQYSDDEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWL 294
QY 300 ASESWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEF-----REWGPQ 344
Db 295 ASEAWASSLIAMPQYFHVVGTTIGFALKAGQIPGRFELKKVHPKSVHNGFAKEFWEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLQEGAKGPLPVDFTLRGH--EESGDRFSNSSAFRPL--CTGDENISSVETPYID 410
QY 383 ----RVVYSVYSAYVAHALHSLLC-----DKSTCTKRVVYPWQLLEEIKVNF 430
Db 411 YTHLRISYNYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRLNFT 470
QY 431 -LLDHQIFFDPQGDVALHLEIVQWQDRSQNP--FQSVASYPL-----QRQLXNIQDIS 482
Db 471 NNMGEQVTFDECGDLVGNYSIINWHLSPEDGSI VKEV-GYNNVYAKGERLFINEEKIL 529
QY 483 WHTVNTTIPMSMCSKRCQSGQKKPV-GIHVCCFECIDCLPGTFLNHTEDEYECQACPNN 541

Db	530	WSGFSREVPFNSCRDCLAGTRKGIIIEGPTCCFECVECPDGEYSDET--DASACNKC	PDD	588
QY	542	EWYQSETSCFKRQLVFLEWHEAPTIAVALLAAGFLSTLAILVIFWRHFQTPIVRSAGG	601	
Db	589	FWNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNR	648	
QY	602	PMCELMLTLLVAYMVVPYVGPVKUSTCLCRQALPFLCFTTICISCIASVRSFQIVCAF--	659	
Db	649	ELSYLLLFSLCCFSSSLFFIGEPOQDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEA	708	
QY	660	KMASRPPRAYSYWVRYQGPYVSMAFITVLKMWIVWIGMLATGLSPTRTDDPKITIVS	719	
Db	709	KIPTSFRHK---WWGLNLQFLLVFLCTFMQIVICVI-WLYTAPPSSYRNQLEDEIIFIT	764	
QY	720	CNPNYRNSLLFNTSLDLLSVVGFSFAYWKGKELPTNYNEAKFITLSMTFYFTSSVSLCTF	779	
Db	765	CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---	821	
QY	780	MSAYSGVLVTIVDLLVTVLNLLAISLG----	YFGPKCYMILFYPERNT	823
Db	822	IPAYASTYGKFSV-AVEVIAILAA5FGLLACIFFNKIYIILFKPSRNT	868	

Search completed: November 30, 2004, 13:54:51
Job time : 213 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:45:48 ; Search time 45 Seconds
(without alignments)
1793.908 Million cell updates/sec

Title: US-10-035-045-21
Perfect score: 4443
Sequence: 1 MGPRAKTICSLFFLLWVLA.....ERNTPAYFNSMIQGYTMRD 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1079.5	24.3	1078	2	A56715 calcium receptor (
2	1075	24.2	1079	2	I59362 calcium/polyvalent
3	1075	24.2	1085	2	S40476 Ca(2+)-sensing rec
4	1064.5	24.0	1088	2	B56715 calcium receptor (
5	1014.5	22.8	858	2	JC7683 taste receptor T1R
6	730	16.4	915	2	A49874 metabotropic gluta
7	720.5	16.2	879	2	JC7160 metabotropic gluta
8	720.5	16.2	879	2	JH0562 metabotropic gluta
9	714	16.1	912	2	JH0563 metabotropic gluta
10	699	15.7	872	2	JH0561 metabotropic gluta
11	682.5	15.4	1171	2	A42916 metabotropic gluta
12	673	15.1	1180	2	JC2132 metabotropic gluta
13	673	15.1	1212	2	JC2131 metabotropic gluta
14	668.5	15.0	871	2	A46742 metabotropic gluta
15	668.5	15.0	908	2	I49142 metabotropic gluta
16	656	14.8	999	2	T27628 hypothetetical prote
17	653.5	14.7	1199	2	A41939 G protein-coupled
18	648.5	14.6	1218	2	S71376 glutamate receptor
19	632	14.2	1267	2	T21340 hypothetetical prote
20	425.5	9.6	551	2	T30806 metabotropic gluta
21	218.5	4.9	921	2	T51136 ionotropic glutama
22	218.5	4.9	923	2	F84732 probable ligand-ga
23	215	4.8	1039	2	T45779 probable glutamate
24	200.5	4.5	953	2	E84732 probable ligand-ga
25	200	4.5	1099	2	T16283 ionotropic gluta
26	186	4.2	950	2	T51134 hypothetetical prote
27	185.5	4.2	925	2	T06128 ionotropic gluta
28	185	4.2	975	2	A84550 probable ligand-ga
29	184	4.1	925	2	T51133 ligand gated chann

30	184	4.1	951	2	T51132 probable glutamate
31	180	4.1	960	2	JE0356 gamma-aminobutyric
32	177.5	4.0	1005	2	S33525 guanylate cyclase
33	176	4.0	933	2	C96495 probable ligand-ga
34	174.5	3.9	912	2	T51131 ligand gated chann
35	169.5	3.8	941	2	T51135 ligand-gated chann
36	168.5	3.8	962	2	D86186 hypothetetical prote
37	160.5	3.6	1679	2	T15968 hypothetetical prote
38	158.5	3.6	976	2	T51137 ionotropic glutama
39	158	3.6	997	2	S33754 glutamate receptor
40	144	3.2	918	2	I58178 glutamate receptor
41	144	3.2	949	2	S19808 glutamate receptor
42	143	3.2	965	2	I51244 N-methyl-D-asparta
43	131.5	3.0	1125	1	OYURCP speract receptor p
44	130.5	2.9	938	2	A46612 N-methyl-D-asparta
45	129.5	2.9	885	2	JN0339 N-methyl-D-asparta

ALIGNMENTS

RESULT 1

A56715
calcium receptor (clone pHPCar-4.0) - human
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text_change 01-Dec-2000
C;Accession: A56715; S49341; A49419; B49419; C49419
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A;Reference number: A56715; MUID:95279439; PMID:7759551
A;Accession: A56715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1078 <GAR>
A;Cross-references: GB:U20759; NID:g683744; PIDN:AAA86503.1; PID:g683745
R;Pearce, S.H.S.; Thakker, R.V.
submitted to the EMBL Data Library, August 1994
A;Reference number: S49341
A;Accession: S49341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>
A;Cross-references: EMBL:X81086
R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, Cell 75, 1297-1303, 1993
A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric
A;Reference number: A49419; MUID:94094324; PMID:7916660
A;Accession: A49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 178-192 <POL>
A;Experimental source: family N
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neor
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
A;Accession: B49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 289-303 <PO2>
A;Experimental source: family E
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and neor
A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
A;Accession: C49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 788-802 <PO3>
A;Experimental source: family J
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and neor
A;Note: sequence extracted from NCBI backbone (NCBIN:142457)

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
Best Local Similarity 31.4%; Pred. No. 1.8e-73;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

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QY 16 WVLAEPAENSDFYLP-----GDYLLGLGFLSHANMKGIVHLNLFLOVPMCKEYEVKVIG 68
Db 8 WVLALTWHTSAYGPDQRAQKGGDIILGGLFPIHF---GVAAKD--QDLKSRPSEVICIR 62

QY 69 YNL-----MQAMRFAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGRWLQAMIFAIEEINSSPALLPNLTGLYRIFDTCNTVSKALEATLSFVAQNKIDS 122

QY 122 LPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRPFA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSNKNQFKS 182

QY 180 LLRTTPSADHHVEAMVQMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICIAPQET 239
Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTTAADDYGRPGIEKFREEAEERDICIIDFSEL 242

QY 240 LPTLQPNQNMNTSEERQLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLNQFTGAVWI 299
Db 243 I-----SQYSDEEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWL 294

QY 300 ASESWAIDPVLHNLTELHGLTFLGITIQSVPIPGFSEF-----REWGPPQ 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKVVHPRKSVHNGFPAKFEWEE 354

QY 345 A-----GPPPLSRTSQSYTCNQCEDNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLQEGAKGPLVDTFLRGH--EESGDRFSNSSTAFRPL--CTGDENISSVETPYID 410

QY 383 ----RVVYSVYSAVYAVAHALHSLGCG-----DKSTCTKRVVYVPWQLLEEIKVKNFT 430
Db 411 YTHLRISYNVYLAIVSYIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRLNFT 470

QY 431 -LLDHQIFFDPQGDVALHLEIVQWQWDRSQNP--FQSVASYYP-----QRQLKNIQDIS 482
Db 471 NNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIIVFKEV-GYNNVYAKKGERLFINKEKIL 529

QY 483 WHTVNTIPTMSCRKRCQSGOKKPV-GIHVCCFECIDCLPGTFELNHTEDYEYECQACPNN 541
Db 530 WSGFSREVFPFNSCRDCLAGTRKGIIEGPTCCFCEVCEPCDGEYSDET-DASACNKCDD 588

QY 542 EWSYQSETSCFKRLQVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPGIALTLFAVLGIFLTAFLVGFIKFRNTPIVKATNR 648

QY 602 PMCFMLTLTLLVAYMVVPVYVGGPKVSTCLCRQALFPLCFFTCISCIAVRSFQIVCAF-- 659
Db 649 ELSYLLLSLLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEA 708

QY 660 KMASRFPFRAYSWVRVYQGPYVSMAPITVLKMVIVIGMLATGLSPTRTDPDPKTIIVS 719
Db 709 KIPTSFRHK---WWGLNLQFLLVFLCTFMQIVICVI-WLYTAPPSSYRNQOELEDEIIFIT 764

QY 720 CNPNVRNLSLLFNTSLDLLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS--F 821

QY 780 MSAYSGVLVTIVDILLVTVLNLAISLG-----YFGPKCYMILFPERNT 823
Db 822 IPAYASTYKGFVS-AVEVIAILAAASFGLLACIFFNKIYIILFKPSRNT 868
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RESULT 2

I59362
calcium/polyvalent cation-sensing receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59362; A55594

R;Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
A;Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals
A;Reference number: I59362; MUID:95241465; PMID:7724534
A;Accession: I59362
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-1079 <RES>
A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:G790578; PIDN:AAC52195.1; PID:G790578
A;Experimental source: striatal
R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995
A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor
A;Reference number: A55594; MUID:95116508; PMID:7816802
A;Accession: A55594
A;Molecule type: mRNA
A;Residues: 1-133, 'X', 135-1079 <RIC>
A;Cross-references: GB:U10354
A;Experimental source: kidney
C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;187-212/Region: hydrophobic
F;613-635/Domain: transmembrane #status predicted <TM1>
F;650-670/Domain: transmembrane #status predicted <TM2>
F;683-700/Domain: transmembrane #status predicted <TM3>
F;725-744/Domain: transmembrane #status predicted <TM4>
F;770-790/Domain: transmembrane #status predicted <TM5>
F;806-828/Domain: transmembrane #status predicted <TM6>
F;841-860/Domain: transmembrane #status predicted <TM7>
F;90,261,287,386,468,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 24.2%; Score 1075; DB 2; Length 1079;
Best Local Similarity 31.4%; Pred. No. 4e-73;
Matches 282; Conservative 166; Mismatches 327; Indels 124; Gaps 33;

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QY 10 SLFFELLWLVAEPAENSDFYLP-----GDYLLGLGFLSHANMKGIVHLNLFLOVPMCKEY 62
Db 9 ALLALAW-----HSSAYGPDQRAQKGGDIILGGLFPIHF---GVAAKD--QDLKSRPE 56

QY 63 EVKVIGYNL-----MQAMRFAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA 116
Db 57 SVECIRYNFRGRWLQAMIFAIEEINSSPALLPNLTGLYRIFDTCNTVSKALEATLSFVA 116

QY 117 -HEDNLLPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDR 173
Db 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSN 176

QY 174 KVRFPALLRTTPSADHHVEAMVQMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDIC 233
Db 177 KNQYKSLRTIPNDEHQATAMADIIEYFRWNWVGTTAADDYGRPGIEKFREEAEERDIC 236

QY 234 IAFQETLPTLQPNQNMNTSEERQLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLNQNF 293
Db 237 IDFSELI-----SQYSDEEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNI 288

QY 294 TGAVWIASESWAIDPVLHNLTELGH-LGTFLGITIQSVPIPGFSEF----- 338
Db 289 TGRIVLASEAWASSSLI-AMPEYFHVVGTTIGFGLKAGQIPGFRFLQKHPRKSVHNGF 347

QY 339 -REWGPPQ-----GPPPLSRTSQSYTCNQCEDNCLNATLSFNTILRLSGE----- 382
Db 348 AKEFWEETFNCHLQEGAKGPLVDTFVRSH--EEGNRLNLSSTAFRPL--CTGDENINS 403

QY 383 -----RVVYSVYSAVYAVAHALHSLGCG-----DKSTCTKRVVYVPWQLLEE 423
Db 404 VETPYMDYEHLRISYNVYLAIVSYIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKH 463

QY 424 IKVKNFT-LLDHQIFFDPQGDVALHLEIVQWQWDRSQNP--FQSVASYYP-----QRQL 475
Db 464 LRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIIVFKEV-GYNNVYAKKGERLF 522
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QY 476 KNIQDISWHTVNNITIPMSMCSKRCQSGQKKPV-GIHVVCCFECIDCLPGTLNHTDEYE 534
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Db 523 INEEKILWSGFSREVPFNSCRDCQAGTRKGIIIGEPTCCFECECPDGEYSGET-DASA 581
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QY 535 CQACPNEWSYQSETSCFKRLVFLEWHEAPTIAVALLAALGFLSTLAILVFWRHFTP 594
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Db 582 CDKCPDDFWSNENHTSIAKEIEFLAWTEPPFGIALTLFAVLGIFLTAFLVGLVFIKPRNT 641
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QY 595 IVRAGGPMCFMLTLLLVAYMVVPVVGPPKVSTCLCRQALPLCLCTICISCIAVRSFQ 654
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 642 IVKATNRELSYLLPSLCCFSSSLFFIGEPODWTCRLRQPAFGISFVLCSILVKTN 701
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 655 IVCAFKMASRFPRAY--SYW-VRYQGYPVSMAFITVLKMVIIVIGMLATGLSPTRTPDP 711
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 702 VLLVFE--AKIPTSFHRKWGNLQ---FLLVFLCTFMQILICIWLTAAPPSSYNHEL 756
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 712 DPKITIVSCNPNYRNLSLNFNTSL---DLLSVVGPSFAYMGKELPTNVNEAKFITLSMTF 768
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 757 EDEIIFITC---HEGSLMALGSLIGYTCLLAACIFFFAFKSRKLPEFNFAKFITFSMLI 813
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 769 YFTSSVSCLTFMSAYSGVLVTIVDLLVTVLNLLAISLG----YFGPKCYMWILFYPERNT 823
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 814 FFIVWIS---FIPAVASTYGKFS-AVEVIAIAASFGLLACIFFNKVYIILFKPSRNT 868
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 3
S40476
Ca(2+)-sensing receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S40476
R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; H Nature 366, 575-580, 1993
A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from h A;Reference number: S40476; MUID:94077182; PMID:8255296
A;Accession: S40476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1085 <BRO>
A;Cross-references: UNIPROT:P35384; GB:S67307; NID:g453108; PIDN:AAB29171.1; PID:g453109

	Query Match	24.2%;	Score 1075;	DB 2;	Length 1085;				
	Best Local Similarity	31.5%;	Pred. No. 4e-73;						
	Matches 279;	Conservative 161;	Mismatches 347;	Indels 98;	Gaps 29;				
QY	11	LFFLLWVLAEP	NSDFYLP	PGDYLLGGLFS	LHANMKGIVHLN	FLOVP---MCKEYEVKVI 67			
DB	11	LAFSTWCTSA	YGPDPQRAK	KGDIILGGLF	PIHFGV-AVKDQDL	KSRPESVECIRYFR-- 67			
QY	68	GYNLQAMRFA	VEEINNDSS	LLPGVLLGYE	IVDVC-YISNNV	QPVLYFLA-HEDNLLPIQ 125			
DB	68	GFRWLQAMIF	AEEINSSPA	LLPNMTLGYR	IFDTCNTVSKA	LEATLSFVAQNKIDSLND 127			
QY	126	E--DYSNVI	SRVAVIGP	DNSESVM	TVANFLSLFLL	POITYSAISDEL	RDKVRFPA	LRT 183	
DB	128	EFCNCSEHI	PSTIAVVG	ATGSGIS	TAVANLLGLF	YIPQVSYASS	RLSNKNQFKS	FLRT 187	
QY	184	TPSADHHVE	AMVQLMLH	FRWNWII	VLVSSDTYGR	DNGQLLGERVA	RDICIAFOET	LPTL 243	
DB	188	IPNDEHQAT	AMADIIEY	FRWNWVG	TIAADDDYGR	PGIEKFREEA	EERDICI	DFSELI --- 244	
QY	244	QPNQNM	TSEERQ	LVTIVDK	LQQSTARVV	VVFSPDLTLYH	FNEVL	RQNFTGAV	WIASES 303
DB	245	---SQYSDE	-EKIQOV	VEVIQNS	TAKVIVVFSS	GGPDLEPLIKE	IVVRNITGR	IWLASEA 299	
QY	304	WAIDPVLHN	LTELGH-LG	TFLGITIQ	SVPIPGFSEF	-----	REWG	PQA-- 345	
DB	300	WASSSLI-AM	PEYFHVVG	TIGFGLKA	QIPGFREF	LQKVHPRKSV	HNGFAKEF	WEETFN 358	
QY	346	-----GPP	PL-----	SRTSQSYT	-----	CNQECN	CINATLS	FN	TLRLSG 381
DB	359	CHLQEGAK	GLPVDV	TLRGLRG	HEEGGARL	SNSP	TAFRPL	CTGE-ENIS	SVETPYMDYTHL-- 415

[illegible]

RESULT 5

JC7683
taste receptor Tlr3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
R;Accession: JC7683
R;Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.
Biochem. Biophys. Res. Commun. 283, 236-242, 2001
A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste.
A;Reference number: JC7683; MUID:21222875; PMID:11322794
A;Contents: tongue
A;Accession: JC7683
A;Molecule type: mRNA
A;Residues: 1-858 <KIT>
A;Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994
C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the si
C;Keywords: transmembrane protein
A;Gene: tlr3
A;Map position: 4
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: transmembrane protein

Db 82 EINNGSALLPGLRLGYDLFDTC-----SEPVVMTKSSLMFLAKVGSQSIAAYCNYTQYQP 136

QY 134 RVAVAVIGPDNSESVMTVANFSLFLPLPQITYSAISDELKDKVRFPPALLRTPPSADHHVEA 193

Db 137 RVLAVIGHPSSELALITGKFFSFFLMPQVSYASMDRLSDRETFFSFRTVPVSDRVQLQA 196

QY 194 MVQLMLHFRMWTIVLVSSDITYGRDNGQLLGERVARRDICIAPQETLPTLQPNQNMTSEE 253

Db 197 VVTLNQFNSWNVAAALGDDDDYGREGLSIFSSLANARGICIAHE---GLVPQHDSTGQQ 252

QY 254 RQRLVTIVDKLQQSTARVVVVVFPDLYLHFFNEVLRQNFETGAVMIASESWAIDPVLHNL 313

Db 253 LGKVLVDLRQVNQSKVQVVVLFASARAVYSLFSYIIHGLSPKVVVASESWLTSDLVMTL 312

QY 314 TELGHLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTS-----QSYTCNQECDNC 366

Db 313 PNIAVGTVLGFLQRGALLPEFSHYVETHALAADPAFCASINAEILDLEEHVMGQRCPRC 372

QY 367 ---LNATLSFNTILRLSERV---VYSVYSAVYAVAHALSHLLGCDKSTC-TKRVVYPWQ 419

Db 373 DDIMLQNLSSGLLQNLASQQLHHQIFATYAAVYSVAQALHNTLQCNVSHCHVSEHVLFWQ 432

QY 420 LLEEIKVNFLLDHQIFPDQGDVALHLEIVQWQDRSQNPFSQSVASYYPQLORQLKNIQ 479

Db 433 LLENMYNMSFHARDLTQLQDAEGNVDMEDLKMVVWQSPTPVLHTVGTG---NGTLQLQ 488

QY 480 DISWHTVNTIPMSMCKRCQSGQKKKPVGIHVCCPECIDCLPGTFLNHTDEYECQACP 539

Db 489 QSKMYWPGNQVPVSCRSQCKDGQVRRVKGFHSCCYDCVDCCKAGSYRKH-PDDFTCTPCN 547

QY 540 NNEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVFWRHFTPIVRS 599

Db 548 QDQWSPEKSTACLPRRPKFLAWGEPVWLSLLLLCLVLGLAALGLSVHHWDSPLVQAS 607

QY 600 GG-PMCFMLTLTLLVAYMVVVPVVPVGVPPKVSTCLCRQALFPLCTTICISCIAVRSFQIVCA 658

Db 608 GGSQFCFGLICLGLFCLSVL-LFPGRPSSASCLAQOPMAHLPLTGCLSTLFLQAAETF-- 664

QY 659 FKWASRFPRAYSYV--RYQGPVVSMAFITVLKMVIIVIGMLA---TGLSPTRTDPDD- 712

Db 665 --VESELPLSWANWLCSYLRGLW--AWLVLLATFVEAALCAWYLIAFPPEVVTWDSVL 719

QY 713 PKITIVSCNPYRNLSLFTSLDILLVSVGFSPAYMGKELPTNVNBAKITLSMTFYFTS 772

Db 720 PTEVLEHCHVRSVWSGLVHTNAMLAFCLGLTFLVQSQPGRYNRARGLTFAMLAYFIT 779

QY 773 SVS---LCTFMSAY-----SGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERN 822

Db 780 WVSFVPELLANVQVAYQPAVQMGAIVCALGILVT-----FHLPKCYVLLWLPKLN 829

QY 823 TPAYF 827

Db 830 TQEFF 834

RESULT 6

A49874

N;Alternate names: metabotropic glutamate receptor 7 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence

C;Accession: A49874; 157954

R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; J. Biol. Chem. 269, 1231-1236, 1994

A;Title: Molecular characterization of a new metabotropic glutamate receptor m

A;Reference number: A49874; MUID:94117433; PMID:8288585

A;Accession: A49874

RESULT 6

A49874

metabotropic glutamate receptor 7 - rat

Metabotropic glutamate receptor, γ 1a
N: Alternate names: metabotropic glutamate receptor mGluR7

N; Alternate names: Metabolic guaiacate
C; Species: Rattus norvegicus (Norway rat)

C;Species: *Rattus norvegicus* (Norway Rat)

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C;Date: 02-Jul-1996 #sequen
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C;Accession: A49874; I57954

R;Okamoto, N.; Hori, S.; Akazawa, C

J. Biol. Chem. 269, 1231-1236, 1994

A;Title: Molecular characterization of a new metabotropic

A: Reference number:

A;Reference Number: A49874, MOID: 54447439, 1112: 02
A:Accession: A49874

A;Accession: A49874
A;Status: preliminary

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 1-915 <RES>

QY 455 WDRSQNPQSVASYPLQRLKNIQDISWHTVNTIPMSMCKRQSQGQKKPVGIHVCC 514
Db 473 HIGGKSYLYKVGHW--AETLYLDVDSIHWS--RNSVPTSCQSDPCAPNEMKMQPGDVCC 528
QY 515 FECIDCLPGTFLNHTDEYEQACPNNEWSYQSETSCFKRLVFLWEHAEPTIAVALLAA 574
Db 529 WICIPCEPYEYL---VDEFTCMDGPGQWPTADLSGCYNLPEDYIRWEDAWAIGPVTIAC 585
QY 575 LGFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLILLVAYMVVPPKYSTCLCRQ 634
Db 586 LGFMCTCIVITVFIKHNTPLVKASGRELCYILLFGVSLSYCMTFFFIAPKSPVICALRR 645
QY 635 ALFPLCFTTICISIAVRSFQIVCAF---KMASRFRPRAYSVWRYQGPYVSMAFITVLKMW 691
Db 646 LGLGTSFAICYSALLTKNCIARIFDGVKNGAQRPKFIS-----PSSQVFI-CLGLI 696
QY 692 IVVIGMLATGL---SPTR--TDPDDPKITIVSCNPNVNSLLFNTSLDLLLLSVVGFSA 746
Db 697 LVQIVMVSVWLILETPGTRRYTLPEKRETVILKCNVK--DSSMLISLTYDVVLVILCTVYA 755
QY 747 YMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFMSAYSGVLVTIIDLIV-TVLNLLAISL 805
Db 756 FKTRKCPENFNEAKFIGFTM---YTTCTIWLAFLEPIF---YVTSSDYRVQTTTMCISVSL 809
QY 806 G-----YFGPKCYMILFYPERN 822
Db 810 SGFVVLGCLFAPKVHIVLFQPKQN 833

RESULT 8
JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0562
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A;Title: A family of metabotropic glutamate receptors.
A;Reference number: JH0561; MUID:92110002; PMID:1309649
A;Accession: JH0562
A;Molecule type: mRNA
A;Residues: 1-879 <TAN>
A;Cross-references: UNIPROT:P31422
A;Experimental source: brain
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F;577-599/Domain: transmembrane #status predicted <TRI>
F;614-634/Domain: transmembrane #status predicted <TII>
F;646-664/Domain: transmembrane #status predicted <III>
F;689-709/Domain: transmembrane #status predicted <TIV>
F;735-756/Domain: transmembrane #status predicted <TRV>
F;770-791/Domain: transmembrane #status predicted <TVI>
F;804-828/Domain: transmembrane #status predicted <VII>
F;209,292,414,439/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 16.2%; Score 720.5; DB 2; Length 879;
Best Local Similarity 26.6%; Pred. No. 2.3e-46;
Matches 230; Conservative 145; Mismatches 353; Indels 137; Gaps 31;

QY 29 LPGDYLLGLFSLHANMKGIVHLNLFQVPMCKEYEVKVIYNLMQAMRFAVEEINNDSSL 88
Db 35 IEGDLVLGLFPINEKGTGTETECGRINEDR-----GIORLEAMLEFAIDEINKDNYL 85
QY 89 LPGVLLGYEIVDVC-----YISNNVQPVLYFLAHEDN---LLP-----IQEDYSNYISRV 135
Db 86 LPGVKLGVIHLDTCRDTYALEQSLFVRASLTKVDEAEYMCPCDGSVAIQE---NIPLLI 142
QY 136 VAVIGPDNSESVMTVANFLSLFLPQITYSAISDELKDRKVRFPALLRTPPSADHHVEAMV 195

Db 143 AGVIGGSYSSVSIQVANLLRLFQIPQISYASTSAKLSDKSRYDYFARTVPPDFYQAKAMA 202
QY 196 QMLHFRWNWIIIVLVSSDITYGRDNGQLLGERVARRDICIATFOETLPTLQPNQNMSTSEERQ 255
Db 203 EILRFFNWTYVSTVASEGDYGETGIEAFQEAEQRLNRCIATAEKVGRSNIRKSYDS----- 258
QY 256 RLVTIVDKLQOSTARVVVVF---SPDLTYHFFNEVLQRNFTGAVWIASWAIDPVLHN 312
Db 259 ---VIRELLQKPNARVVVLFMRSDDSRELIAAANRV-NASFT---WVASDGGWAQESIVK 311
QY 313 LTELGLHGLTGLGITIQSUPI-----PGSEFREWGPQAGPPLSRSTS 354
Db 312 GSEHVAYGA-ITLELASHPVRFQDRYFQSLNPNYNNHRNPWFRDFWE----- 356
QY 355 QSYTCN-----QECDCNCLNATLSFNTILRLSGRVVYSVAVYAVAHALHSLLG-- 404
Db 357 QKFCQSLQNKRNHRQVCDKHLAIDSS-----NYEQESKIMFVNNAVYAMAHALHKMQRTL 411
QY 405 CDKST--CTKRVVYPWQLL--EEIKVNFIL-----LDHQIFFDPQGDVALHLEIVQW 453
Db 412 CPNTTKLCDAMKILDGKKLYKEYLLKINFAPFNPNKGADSVKEDTFDGMGRYVFNIL 471
QY 454 QWDRSQNPQSVASYPLQRLKNIQDISWHTVNTIPMSMCKRQSQGQKKPVGIHVCC 513
Db 472 QQTGGKYSYLYKVGHW--AETLSLDVDSIHWS--RNSVPTSCQSDPCAPNEMKMQPGDVC 527
QY 514 CFECIDCLPGTFLNHTDEYEQACPNNEWSYQSETSCFKRLVFLWEHAEPTIAVALLA 573
Db 528 CWICIPCEPYEYL---VDEFTCMDGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVTIA 584
QY 574 ALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLILLVAYMVVPPKYSTCLCR 633
Db 585 CLGFLCTCIVITVFIKHNTPLVKASGRELCYILLFGVSLSYCMTFFFIAPKSPVICALR 644
QY 634 QALFPLCFTTICISIAVRSFQIVCAF---KMASRFRPRAYSVWRYQGPYVSMAFITVLK 690
Db 645 RLGLGTSFAICYSALLTKNCIARIFDGVKNGAQRPKFIS-----PSSQVFI-CLGL 695
QY 691 VIVVIGMLATGL---SPTR--TDPDDPKITIVSCNPNVNSLLFNTSLDLLLLSVVGFSA 745
Db 696 ILVQIVMVSVWLILETPGTRRYTLPEKRETVILKCNVK--DSSMLISLTYDVVLVILCTVY 754
QY 746 AYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFMSAYSGVLVTIIDLIV-TVLNLLAIS 804
Db 755 AFKTRKCPENFNEAKFIGFTM---YTTCTIWLAFLEPIF---YVTSSDYRVQTTTMCISVS 808
QY 805 LG-----YFGPKCYMILFYPERN 822
Db 809 LSGFVVLGCLFAPKVHIVLFQPKQN 833

RESULT 9
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0563; I58149
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A;Title: A family of metabotropic glutamate receptors.
A;Reference number: JH0561; MUID:92110002; PMID:1309649
A;Accession: JH0563
A;Molecule type: mRNA
A;Residues: 1-912 <TAN>
A;Cross-references: UNIPROT:P31423
A;Experimental source: brain
R;O'Hara, P.J.; Sheppard, P.O.; Thogersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V
Neuron 11, 41-52, 1993
A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to ba
A;Reference number: I58149; MUID:93332699; PMID:8338667
A;Accession: I58149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA


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QY 350 LSRTSQSYTCNQECNCLNATLSFNLTILRLSGERVVSVYSAYVAHAHLSL--LGCDK 407
Db 346 REFWEERFHCSFRQDCAAHSL---RAVPFEQESKMFVNVAVYAMAHALHNHRLCPN 402
QY 408 ST--C-TKRVPVYPMQLLEE-IWKVNFTL-----LDHQIFPDQGDVALHLEIVQW-QWD 456
Db 403 TTHLCDAMRPVNGRRLYKDFVLNVKFDAPFRPADTDEVRFRDGRGIGRYNIFTYLRAG 462
QY 457 RSQNPFFQSVASYPLQRLKNIQDISWHTVN-NTIPMSMCKRCQSGQKKKPVGIHVCCF 515
Db 463 SGRVRYQKVG--YWAEGTLTDTSPFPWASPSAGPLPASRCSEPCLONEVKSVPQGEVCCW 520
QY 516 ECIDCLPGTFLNHTEDEYEQACPNNEWSYQSETSCFKRQLVFELEWHEAPTIAVALLAAL 575
Db 521 LCIPCQP--YEYRLDEFTCADCGLYWPNASLTGCFELPQEIYIRWGDAWAVGPVTIACL 577
QY 576 GFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLTLLVAYMVVVPVYVGGPKVSTCLCRQA 635
Db 578 GALATLFLVLFVVRHNATPVVKASGRELCYILLGGVFLCYCMTFVFIKPSSTAVCTLRRL 637
QY 636 LFPLCFTTICISCIASVRSFQIVCAFKMASRFPRAYSYVRYQGPVVSMAFITVL---KMVI 692
Db 638 GLGTAFSVCVYSALLTKTNRIARIFGGA---REGAQRPRFISPASQVAICLALISGQLLI 693
QY 693 VVIGMLATGLSPTRTPDDPKITIVSCNPNYRN-SLLENTSLDLLSVVGFSPAYMCKE 751
Db 694 VAAWLVEAPGTGKETAPERREVTLR--NHRDASMLGSLAYNVLLIALCTLYAFKTRK 751
QY 752 LPTNNYNEAKFITLSM-----TFYFTSS-----VSLCTFMSAYSGLVLTIVDL 793
Db 752 CPENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQTTMCVSVLSGSV----- 804
QY 794 LVTVLNLLAISLGYFGPKCYMILFYPERNTPAY 826
Db 805 ---VLGCL-----FAPKLHIILFQPKQNVVSH 828

RESULT 11
A42916
metabotropic glutamate receptor mGluR5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42916
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 co
A;Reference number: A42916; MUID:92317054; PMID:1320017
A;Accession: A42916
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1171 <ABE>
A;Cross-references: UNIPROT:P31424; GB:D10891; NID:G220813; PIDN:BAA01711.1; PID:d100218
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIIP:107750)
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.4%; Score 682.5; DB 2; Length 1171;
Best Local Similarity 25.5%; Pred. No. 2.6e-43;
Matches 226; Conservative 153; Mismatches 344; Indels 165; Gaps 31;

QY 28 YLPGDYLLGGLFSLHANMKGIVHLNLFQVPMCKEYEVKV-----IGYNLMQAMRFAVEE 81
Db 30 HMPGDIIIGALFSVH-----H-----QPTVDKXHERKCGAVREQIGIQRVEAMLHTLER 78
QY 82 INNDSSLLPGVLLGYEIVDVCIYS-----NNVQPVLYFLAHDNLLPIQEDYSNYIS 133
Db 79 INSDPTLLENITLGCIEIRDSCWHSVALEQSIIEFIRDSLISSEEEGLVRCVDGSSSFRS 138
QY 134 R--VVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKDKVRFPALLRTPSADHHV 191
Db 139 KKPIGVIGPGSSSVAIQVQNLQLFNIPQIAYSATSMDLSKTLFKYFMRVWPVPSDAQQA 198
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QY 192 EAMVQLMLHFRWNIIIVLVSSDITYGRDNGQLLGERVARRDICIADFQETLFTLPQNQNMTS 251
Db 199 RAMVDIVKRYNWTYVSAVHTEGNYGESGMEAFKDMAKSAKEGICIAHSYKI-----YSN 250
QY 252 EERQLVTIVDKLQ--STARVVVVFSPDLTLYHFFNEVLQRNFTGA-VWIASESWAIDP 308
Db 251 AGEQSFDKLLKKLRSHLPKARVWACFCEGTMVTRGLLMAMRRLGLAGEFLLGLSGDGA--- 307
QY 309 VLHNLTELGLGTFLGITI--QSVPI-----PGSEFEFREGPQAGPP 348
Db 308 DRYDVTGQYQREAVGGITIKLQSPDVKKWFDDYVLKLRPETNLRNPWFQEFWQHRFQCRLE 367
QY 349 PLSRTSQSYTCNQECNCLNATLSFNLTILRLSGERVVYS---VYSAVYAVAHALHSLLG 404
Db 368 GFAQENSKY--NKTC-----NSSLTLRTHHVQDSKMGFVINAIYSMAYGLHNM-- 413
QY 405 CDKSTC-----TKRVVYPWQLLEEIWKNFT-LLDHQIFFDPQGDVALHLEIVQWQ- 454
Db 414 -QMSLCPGYAGLCDAMKPIDGRKLLDSLMTKNTFTGSGDMILFDENGDSPGRYEIMNPK 472
QY 455 -----WDRSQNPFFQSASYYPLQRLKNIQDISWHTVNNTIPMSMCKRCQS 501
Db 473 MGKDYFDYINVGSWDNG-----ELKMDDEDEVWSKKNNII-RSVCSEPC 516
QY 502 GQ-----KKKPVGIHVCCFECIDCLPGTFLNHTEDEYEQACPNNEWSYQSETSCFKRQLV 557
Db 517 GQIKVIRKGEVS---CCWTCCTPCKENEYV---FDEYTCACQLGSWPTDDLGTCDLIPVQ 570
QY 558 FLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFMLTLTLLVAYMV 617
Db 571 YLRWGDPEPIAAVVFACLGGLATLFTVTIIFIIYRDTPVVKSSSRELICYIILAGICLG 630
QY 618 VPVYVGGPKVSTCLCRQALPPLCFTTICISCIASVRSFQIVCAF-----KMASRFPRAYSY 672
Db 631 TFCLIAKPKQIYCYLQIRIGLSPAMSYSALVTKTNRILAGSKKIKCTKKPRFMSAC 690
QY 673 VRYQGPVVSMAFITVLKMWIVVIGMLATGLSPTRTPDDPKITIVSCNPNYRN-SLLEN 731
Db 691 AQ-----LVIAFILICIQGLIIVALFI-----MEPPD-----IMHDYPSIREVYLICN 733
QY 732 TSIDLILLSVVGFSS-----FAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSA 782
Db 734 TTNLGVVTPLGYNGLLILSCTFYAFKTRNVNPNANFNEAKVIATM---YTTCTIIWLAFVPI 790
QY 783 YSGVLVTIVDILLVTVLNLALISLG-YFGPKCYMILFYPERNTPAYFNS 829
Db 791 YFGSNYKIITMCFSVSLSATVALGCMFVPVKVYIILAKPERNVRSAFTT 838

RESULT 12
JC2132
metabotropic glutamate receptor 5 A - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C;Accession: JC2132
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A;Title: Molecular cloning and the functional expression of two isoforms of human metab
A;Reference number: JC2131; MUID:94197696; PMID:7908515
A;Accession: JC2132
A;Molecule type: mRNA
A;Residues: 1-1180 <MIN>
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F;580-604/Domain: transmembrane #status predicted <TM1>
F;617-637/Domain: transmembrane #status predicted <TM2>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;694-714/Domain: transmembrane #status predicted <TM4>
F;738-759/Domain: transmembrane #status predicted <TM5>
F;773-794/Domain: transmembrane #status predicted <TM6>
F;803-827/Domain: transmembrane #status predicted <TM7>

Query Match 15.1%; Score 673; DB 2; Length 1180;
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Best Local Similarity		25.4%;	Pred. No. 1.4e-42;		
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QY	28	YLPGDYLLGGLFSLHANMKGIVHLNFILOVPMCKEYEVKV-----IGYNLMQAMREFAVEE	81		
Db	30	HMPGDIIGALFSVH-----H-----OPTVDKVHERKCGAVREQYGIQRVEAMLHTLER	78		
QY	82	INNDSSLLPGVLLGVEIVDVCIYSN-NVQPVLYFLAHEDNLLPIQED-----YSN	130		
Db	79	INSDPTLLPNITLGCIRDSCWHSVALEQSIIEFI--RDSLISSEEEGLVRCVDDGSSSS	136		
QY	131	YISR--VVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPALLRTPPSAD	188		
Db	137	FRSKKPIVGIVGPGSSVAIQVQLLQFNIPQIAYSATSMDSLTKTLFKYFMRVVPDPA	196		
QY	189	HHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIATQETLPTLPQNPQN	248		
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QY	249	MTSEERQRLVTIIVDKLQOS-----TARVVVVFSPDLTYLHFFNEVLRNQFTGA-VMIAS	301		
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QY	302	ESWAIDPVLHNLTELGHGLTFLGITI--QSVPI-----PGSESEPREW	341		
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QY	342	GPQAGPPPLSRTSQSYTCNOECDNCLNATLSFNTILRLSGERVVYS-----VYSAYAVAH	397		
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Db	685	PRFMSACAQ----LVIAFILICIQIGIIVALFI-----MEPPD---IMHDYPSIR	727		
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 A;Accession: JC2131
 A;Molecule type: mRNA
 A;Residues: 1-1212 <MIN>
 C;Comment: This protein is coupled to guanine nucleotide binding proteins.
 C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
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 F;803-827/Domain: transmembrane #status predicted <TM7>

Abstract: Molecular cloning and the functional expression of two isoforms of human metabo

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 09:16:39 ; Search time 1068 Seconds
(without alignments)
17512.816 Million cell updates/sec

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Perfect score: 3563
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues 8269772

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3563	100.0	3563	6	ABN84919 Human tas
3	3403.8	95.5	8001	6	AAL38463 Genomic D
4	3403.8	95.5	8001	9	ACA62667
5	3398.6	95.4	4256	10	ADC86148 Human GPC
6	3088.2	86.7	3200	10	ADK90723 Human tas
7	2965.4	83.2	3115	8	ABZ42555 Human G p
8	2687	75.4	2687	5	AAD17508
9	2157.4	60.6	2685	12	ADI40945
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12	2086.2	58.6	3446	10	ADJ93108 Human G-c
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24	1893.8	53.2	2559	6	AAS97395	Aas97395 Human SAC
25	1893.8	53.2	2559	12	ADG19753	Adg19753 G protein
26	1893.8	53.2	2559	12	ADM15734	Adm15734 Human SAC
27	1885	52.9	2553	5	AAD17509	Aad17509 Human tas
28	1885	52.9	2553	10	ADK90738	Adk90738 Human tas
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31	1787.6	50.2	2415	10	ADC12739	Adc12739 Human GPC
32	1747.4	49.0	2490	12	ADI40943	Adi40943 Human G p
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35	1312.8	36.8	11809	6	AAS97394	Aas97394 Murine SA
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38	1291	36.2	3200	10	ADK90731	Adk90731 Mouse tas
39	1190	33.4	1788	6	AAD34459	Aad34459 Human GPC
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43	835.6	23.5	2577	5	AAD17514	Aad17514 Rat taste
44	835.6	23.5	2577	6	ABN84925	Abn84925 Rat taste
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ALIGNMENTS

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AC	AAD17517;
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DT	10-DEC-2001 (first entry)
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DE	Human taste receptor, hTIR3 full-length genomic DNA.
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KW	Human; taste-cell-specific G protein-coupled receptor; TIR3; drug;
KW	genetic modulation; pharmaceutical; taste sensation; food industry;
KW	chemosensory transduction; chromosome 1p36.2-1p36.33; ds.
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OS	Homo sapiens.
XX	
FH	Key
FT	CDS
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WO200166563-A2.

13-SEP-2001.

07-MAR-2001; 2001WO-US007265.

07-MAR-2000; 2000US-0187546P.
07-APR-2000; 2000US-0195536P.
06-JUN-2000; 2000US-0209840P.
23-JUN-2000; 2000US-0214213P.
17-AUG-2000; 2000US-0226448P.
03-JAN-2001; 2001US-0259227P.

(SENO-) SENOMYX INC.

Adler JE, Zozulya S, O'connell SM, Li X, Staszewski L;

WPI; 2001-582267/65.

P-PSDB; AAE10366.

New mammalian taste-cell-specific G protein-coupled receptor polypeptides for identifying compounds that modulate taste signaling are useful in food, to modulate the sweet taste of foods or drugs.

Claim 1; Page 71-72; 119pp; English.

The invention relates to mammalian taste-cell-specific G protein-coupled receptors, T1R and their corresponding cDNA molecules. Taste receptors, T1R are useful for screening compounds which are used to activate or modulate chemosensory transduction, such as taste sensation. The identification and isolation of novel taste receptors and genetic signalling molecules allow for new methods of chemical and taste modulation of taste transduction pathways. The taste modulating compounds are useful in pharmaceuticals and food industries to improve the taste of a variety of consumer products, or to block undesirable tastes, e.g., in certain pharmaceuticals. T1R,s are also useful in biochemical assay for identifying tastant (T1R) ligands having binding specificity for T1R involved in taste signalling. The present sequence is human taste-cell-specific G protein-coupled receptor, hT1R3 full-length genomic DNA. Human T1R3 gene is localised on chromosome 1p36.2-1p36.33

Sequence 3563 BP; 545 A; 1214 C; 1166 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 3563; DB 5; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC ABN84919;
XX
DT 25-NOV-2002 (first entry)
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XX
KW hT1R3; T1R3; T1R; G-protein coupled receptor; receptor; human; taste;
KW sweet; gene; ds.
OS Homo sapiens.

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XX WO200264631-A2.
XX
PN 22-AUG-2002.
XX
PD 03-JAN-2002; 2002WO-US000198.
XX
PF 03-JAN-2001; 2001US-0259227P.
PR 19-APR-2001; 2001US-0284547P.
XX
PA (SENO-) SENOMYX INC.
XX

PI Adler JE, Li X, Staszewski L, O'Connell S, Zozulya S;
XX WPI; 2002-666991/71.
DR P-PSDB; ABB79827.
XX
PT Novel mammalian taste-cell specific G protein-coupled receptors active in
PT taste signaling, useful for representing the perception of taste and for
PT predicting the perception of taste in a mammal.
XX
PS Claim 1; Page 72-74; 132pp; English.
XX
CC The present sequence is that of genomic DNA encoding a novel human G-
CC protein coupled receptor (GPCR), designated hT1R3, that is involved in
CC sweet taste transduction. The invention provides a new family of taste
CC cell-specific GPCRs, the T1Rs, active in taste perception. Genomic DNAs
CC and cDNAs encoding the receptors are described, along with methods for
CC isolating T1R genes and for isolating and expressing T1R polypeptides.
CC Methods for representing taste perception of a particular taste stimulus
CC in a mammal, including a human, are also described, as are methods for
CC generating novel molecules or combinations of molecules that elicit a
CC predetermined taste perception in a mammal, and methods for stimulating
CC one or more tastes. Methods for stimulating or blocking taste perception
CC are also disclosed, as are methods of screening for modulators of these
CC novel taste cell-specific GPCRs. Such modulators are useful for
CC pharmacological, chemical and genetic modulation of taste signalling
CC pathways. They can be used in the food or pharmaceutical industries to
CC customize taste, e.g. to modulate the sweet tastes of foods or drugs. T1R
CC nucleic acids and the proteins they encode can be used as probes to
CC dissect taste-induced behaviours. Chromosome localisation of the genes
CC encoding human T1Rs can be used to identify diseases, mutations, and
CC traits caused by and associated with T1R family members. T1R genes and
CC their homologues are useful tools for identifying chemosensory receptor
CC cells, for forensics and paternity determinations, and for examining
CC taste transduction
XX
SQ Sequence 3563 BP; 545 A; 1214 C; 1166 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 3563; DB 6; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 1621 CTCTGTCTACGACAGCTGTGTATAGCTGGCCCCAGGCCCTGCACAACACTCTTCAAGTCAA 1680
QY 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCCGGAGATGG 1740
Db 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCCGGAGATGG 1740
QY 1741 GGGTGTGCTGCTCTCTGCAATGTGCCAGGCCACACAGGCACGGCCACACCGCCTGAGCTGG 1800
Db 1741 GGGTGTGCTGCTCTCTGCAATGTGCCAGGCCACACAGGCACGGCCACACCGCCTGAGCTGG 1800
QY 1801 AGGTGGCTGGCGGCTCAGCCCCCTGCCCCCGCCGCGAGCTCCTGGAGAACATGTACAACCT 1860
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QY 1861 GACCTTCCACGTGGCGGGCTGCCGCTGCCGCTGCCGCTTCGACAGACGGGAAAACGTGGACATGA 1920
Db 1861 GACCTTCCACGTGGCGGGCTGCCGCTGCCGCTTCGACAGACGGGAAAACGTGGACATGA 1920
QY 1921 GTACGACCTGAAGCTGTGGGTGGGAGGGCTCAGTCCCAGGCTCCACGACGTGGGCAG 1980
Db 1921 GTACGACCTGAAGCTGTGGGTGGGAGGGCTCAGTCCCAGGCTCCACGACGTGGGCAG 1980
QY 1981 GTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGCTCTGACAAACCA 2040
Db 1981 GTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGCTCTGACAAACCA 2040
QY 2041 GGTGAGGTGAGGGTGGGTGGTGGCAGGCTGCCGCTGGTAGCCCCCGCGGACGGCGCAGC 2100
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Db 2221 CGCCGGGTCAAGGGGTTCCACTCTGCTGCTACGACTGTGTGGA 2280
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Db 2521 CCGGCTGTGCTGCTGCTCTGCTGCTGAGCCTGGCGCTGGGCTTGTGCTGGCTGCT 2580
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Db 2821 AGCTGGCAGACCCGGTGCCTGAGTGGCTGCCTGCGGGGCCCTGGGCTGGTGGTGGTCTG 2880

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Db 2941 GTGGTGACGACTGGCACATGTGCCCCACGGAGCGCTGGTGGCTGCCCCACACGCTCC 3000

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Db 3001 TGGGTGAGCTTCGGCCTAGCGACGCCACCAATGCCAGCTGGCCTTCTCTGCTTCCCTG 3060

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Db 3061 GGCACTTCTGCTGGTGCGGAGCGCGGGCTGCTACAACCGTGGCCTGCGCTCACCTTT 3120

QY 3121 GCCATGCTGGCCTACTTCACTACCTGGGTCTCCTTTGTGCCCCCTCCTGGCCAATGTGCAG 3180

Db 3121 GCCATGCTGGCCTACTTCACTACCTGGGTCTCCTTTGTGCCCCCTCCTGGCCAATGTGCAG 3180

QY 3181 GTGGTCTCAGGCCCGCGTGCAGATGGCGGCCCTCCTGCTGTGTCTGGGCAATCCCTG 3240

Db 3181 GTGGTCTCAGGCCCGCGTGCAGATGGCGGCCCTCCTGCTGTGTCTGGGCAATCCCTG 3240

QY 3241 GCTGCTTCCACCTGCCAGGTGTACCTGTCTCATGCGGAGCGCGGCTCAACACCCCTC 3300

Db 3241 GCTGCTTCCACCTGCCAGGTGTACCTGTCTCATGCGGAGCGCGGCTCAACACCCCTC 3300

QY 3301 GAGTTCTTCTGGAGGGGCCCTGGGGATGCCCAAGGCCAGATGACGGGAACACAGGA 3360

Db 3301 GAGTTCTTCTGGAGGGGCCCTGGGGATGCCCAAGGCCAGATGACGGGAACACAGGA 3360

QY 3361 AATCAGGGGAAACATGAGTGACCCCAACCTGTGATCTCAGCCCCGGTGAACCCAGACTTA 3420

Db 3361 AATCAGGGGAAACATGAGTGACCCCAACCTGTGATCTCAGCCCCGGTGAACCCAGACTTA 3420

QY 3421 GCTGCGATCCCCCAAGCCAGCAATGACCGTGTCTCGTACAGAGACCTCCCGCTCT 3480

Db 3421 GCTGCGATCCCCCAAGCCAGCAATGACCGTGTCTCGTACAGAGACCTCCCGCTCT 3480

QY 3481 AGGTTCTGACCCAGGTTGTCTCCTGACCCCTGACCCCAAGCCAGTGAAGCCCTAGGCTGGAGC 3540

Db 3481 AGGTTCTGACCCAGGTTGTCTCCTGACCCCTGACCCCAAGCCAGTGAAGCCCTAGGCTGGAGC 3540

QY 3541 ACGTGGACACCCCTGTGACCATC 3563

Db 3541 ACGTGGACACCCCTGTGACCATC 3563

RESULT 3
AAL38463
ID AAL38463 standard; DNA; 8001 BP.
XX
AC AAL38463;
XX
DT 15-AUG-2002 (first entry)
XX
DE Genomic DNA encoding a human G-protein coupled receptor (GPCR).
XX

KW G-protein coupled receptor; GPCR; gene chip; human; immune response;
KW chromosomal position; transgenic animal; gene therapy; gene; ds.
XX Homo sapiens.
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FH Key Location/Qualifiers
FT allele replace(406,C)
FT *tag= m
FT allele replace(852,C)
FT *tag= n
FT allele replace(897,A)
FT *tag= o
FT allele replace(1433,T)
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FT /note= "This coding sequence contains 5 introns"
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FT 2309..2409
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FT allele replace(7028,A)
FT *tag= r
XX WO200230981-A1.
XX 18-APR-2002.
XX 13-MAR-2001; 2001WO-US007832.
XX 10-OCT-2000; 2000US-00684393.
XX (PEKE) PE CORP NY.
XX Wei M, Zhong W, Ketchum KA, Difrancesco V, Beasley EM;
XX WPI; 2002-444173/47.
XX P-PSDB; AAO21501.
XX Novel G protein coupled receptor, useful for raising antibodies, to
XX elicit immune response, and as a reagent in assays designed to
PT

PT quantitatively determine levels of protein in biological samples.

XX Disclosure; Fig 3; 82pp; English.

CC The invention relates to an isolated G-protein coupled receptor (GPCR) polypeptide, comprising an 852 residue amino acid sequence, given in the CC specification, an allelic variant or ortholog of the protein, or a CC fragment comprising at least 10 contiguous amino acids of the protein. CC GPCR is useful for identifying a modulator of GPCR and an agent that CC binds to GPCR. GPCR and a gene chip comprising GPCR are useful as models CC for the development of human therapeutic agents. GPCR is useful for CC raising antibodies, to elicit immune response, as a reagent in assays CC designed to quantitatively determine levels of protein in biological CC samples, and as markers for tissues in which the corresponding protein is CC preferentially expressed. A gene chip containing GPCR is also useful as a CC probe for determining the chromosomal positions of nucleic acid molecules CC by means of in situ hybridisation, in making vectors containing the gene CC regulatory regions of a gene chip containing GPCR, for designing CC ribozymes, in making vectors that express GPCR, and for constructing host CC cells and transgenic animals expressing nucleic acid molecules and CC peptides. A host cell containing GPCR is useful for conducting cell-based CC assays involving GPCR protein or its fragments, and for identifying CC protein mutants in which these function is affected. The polynucleotide CC encoding GPCR can be used to treat disorders by gene therapy. This CC polynucleotide sequence represents The genomic DNA encoding the human G- CC protein coupled receptor of the invention

xx Sequence 8001 BP; 1291 A; 2630 C; 2623 G; 1457 T; 0 U; 0 Other;

Query Match 95.5%; Score 3403.8; DB 6; Length 8001;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3489; Conservative 0; Mismatches 22; Indels 52; Gaps 2;

QY	1	AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGCCCCAGGAAGCGA	60
Db	1908	AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGCCCCAGGAAGCGA	1967
QY	61	GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGGCAAGGTTTGTCTAAACAAA	120
Db	1968	GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGGCAAGGTTTGTCTAAACAAA	2027
QY	121	TCCTCTGCCCCGCTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC	180
Db	2028	TCCTCTGCCCCGCTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC	2087
QY	181	CTGCCGTGCTGTGGAAAGTTGCCTCTTGCCATGCTGGGCCCTGTGCTCCTGGGCCCTCAGC	240
Db	2088	CTGCCGTGCTGTGGAAAGTTGCCTCTGCCATGCTGGGCCCTGTGCTCCTGGGCCCTCAGC	2147
QY	241	CTCTGGGCTCTCCTGCAACCTGGGACGGGGCCCCATGTGCTCCTGACAGCAACTTAGG	300
Db	2148	CTCTGGGCTCTCCTGCAACCTGGGACGGGGCCCCATGTGCTCCTGACAGCAACTTAGG	2207
QY	301	ATGAAGGGGGACTACGTGCTGGGGGGGTGTTCCCGCTGGGCGAGGCCGAGAGGCTGGC	360
Db	2208	ATGAAGGGGGACTACGTGCTGGGGGGGTGTTCCCGCTGGGCGAGGCCGAGAGGCTGGC	2267
QY	361	CTCCGCAGCCGGACACGGCCAGCAGCCCTGTGTGACCCAGGTACAGAGTGGGACGGCC	420
Db	2268	CTCCGCAGCCGGACACGGCCAGCAGCCCTGTGTGACCCAGGTACAGAGTGGGACGGCC	2327
QY	421	TGGGTGCGGGTCAGGGTGACAGGTCTGGGGTGCTCTGAGCTGGGGCCGAGGTGGCCAT	480
Db	2328	TGGGTGCGGGTCAGGGTGACAGGTCTGGGGTGCTCTGAGCTGGGGCCGAGGTGGCCAT	2387
QY	481	CTGCGGTTCTGTGTGGCCCCCAGGTTCTCCTCAACGGCCCTGCTCTGGGCACCTGGCCATGA	540
Db	2388	CTGCGGTTCTGTGTGGCCCCCAGGTTCTCCTCAACGGCCCTGCTCTGGGCACCTGGCCATGA	2447
QY	541	AAATGGCCGTGGAGGAGATCAACAAAGTCCGATCTGCTGCCCGGGCTGCGCCTGGGCT	600
Db	2448	AAATGGCCGTGGAGGAGATCAACAAAGTCCGATCTGCTGCCCGGGCTGCGCCTGGGCT	2507

QY	601	ACGACCTCTTTGATACGTCTCGGAGCCCTGTGGTGGCCATGAAGCCCGCCTCATGTTCC	660
Db	2508	ACGACCTCTTTGATACGTCTCGGAGCCCTGTGGTGGCCATGAAGCCCGCCTCATGTTCC	2567
QY	661	TGGCCAAGCAGGCGGACATCGCCGCTACTGCAACTACAGAGTACAGCCCC	720
Db	2568	TGGCCAAGCAGGCGGACATCGCCGCTACTGCAACTACAGAGTACAGCCCC	2627
QY	721	GTGTGCTGCTCATCGGGCCCCACTGCTCAGAGTCTGCCATGTTGTCACCGCAAGTTCT	780
Db	2628	GTGTGCTGCTCATCGGGCCCCACTGCTCAGAGTCTGCCATGTTGTCACCGCAAGTTCT	2687
QY	781	TCAGCTTCTTCTCATGCCCCAGTGGGGCGCCCCACCATCACCCACCCCAACCAACC	840
Db	2688	TCAGCTTCTTCTCATGCCCCAGTGGGGCGCCCCACCATCACCCACCCCAACCAACC	2747
QY	841	CCTGCCCGTGGAGCCCTTGTGTGAGGAGATGCTATCATGCAACCCACCCAGCCCTGC	900
Db	2748	CTGCCCGTGGAG--CCCCTGTGTGAGGAGATGCCT-----	2781
QY	901	CCTGGGAGCCCTGTGTGAGGAGATGCTTCTGGCCCTTGCAGGTACAGGTGCTAGCAT	960
Db	2782	-----CTTGGCCCTTGCAGGTACAGGTGCTAGCAT	2815
QY	961	GGAGCTGCTGAGCGCCCGGAGACCTTCCCTCCTTCTTCGACACCGTCCCGAGCAGCG	1020
Db	2816	GGAGCTGCTGAGCGCCCGGAGACCTTCCCTCCTTCTTCGACACCGTCCCGAGCAGCG	2875
QY	1021	TGTGAGCTGACGGCCCGCGAGCTGTGAGGAGTTCGGCTGGAACCTGGTGGCCGC	1080
Db	2876	TGTGAGCTGACGGCCCGCGAGCTGTGAGGAGTTCGGCTGGAACCTGGTGGCCGC	2935
QY	1081	CCTGGGCAGCGACGACGAGTACGGCCGGCAGGGCCTGAGCATTTCTCGGCCCTGGCCGC	1140
Db	2936	CCTGGGCAGCGACGACGAGTACGGCCGGCAGGGCCTGAGCATTTCTCGGCCCTGGCCGC	2995
QY	1141	GGCAGCGGCATCTGATCGCGCACGAGGGCCTGGTGGCTGCCCTGCCGATGACTC	1200
Db	2996	GGCAGCGGCATCTGATCGCGCACGAGGGCCTGGTGGCTGCCCTGCCGATGACTC	3055
QY	1201	GCGGCTGGGAAGGTGACAGGACGTCTCTGCACCAAGGTGAACAGAGCAGCGTGAGGTGGT	1260
Db	3056	GCGGCTGGGAAGGTGACAGGACGTCTCTGCACCAAGGTGAACAGAGCAGCGTGAGGTGGT	3115
QY	1261	GCTGCTGTTGCGCTCGTGCACGCCGCCACGCCCTCTTCAACTACAGCATCAGCAGCAG	1320
Db	3116	GCTGCTGTTGCGCTCGTGCACGCCGCCACGCCCTCTTCAACTACAGCATCAGCAGCAG	3175
QY	1321	GCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCTGGCTGACCTCTGACCTGGTTCATGG	1380
Db	3176	GCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCTGGCTGACCTCTGACCTGGTTCATGG	3235
QY	1381	GCTGCCCGCATGSCCCAGATGGGCACGGTGTGGCTTCTTCCAGAGGGGTGCCCCAGCT	1440
Db	3236	GCTGCCCGCATGSCCCAGATGGGCACGGTGTGGCTTCTTCCAGAGGGGTGCCCCAGCT	3295
QY	1441	GCACGAGTTCCCGCAGTACGTGAAGACGACCTGGCCCTGGCCACCGACCCGGCCTTCTG	1500
Db	3296	GCACGAGTTCCCGCAGTACGTGAAGACGACCTGGCCCTGGCCACCGACCCGGCCTTCTG	3355
QY	1501	CTCTGCCCTGGGCGAGAGGGGTCAGGGTCTGGAGGAGGACGTGGTGGGCGAGCGCTGCC	1560
Db	3356	CTCTGCCCTGGGCGAGAGGGGTCAGGGTCTGGAGGAGGACGTGGTGGGCGAGCGCTGCC	3415
QY	1561	GCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCACCACAGACGTT	1620
Db	3416	GCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCACCACAGACGTT	3475
QY	1621	CTCTGTCTACGAGCTGTGTATAGCTGGCCCGAGGCCCTGCACAACTCTTTCAGTGCAA	1680
Db	3476	CTCTGTCTACGAGCTGTGTATAGCTGGCCCGAGGCCCTGCACAACTCTTTCAGTGCAA	3535
QY	1681	CGCCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	1740

Db 3536 CGCCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG 3595
QY 1741 GGGTGTGCTGTCTCTGTCATGTGCCAGGCCACAGGCCACGGCCACCCACGCTGAGCTGG 1800
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QY 1801 AGGTGGCTGGCGGCTCAGCCCGCTCCCCCGCCGAGCTCCTGGAGAACATGTACAACTT 1860
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Db 3776 GTACGACCTGAAGCTGTGGTGTGGCAGGGCTCAGTCCCAGGCTCCACGACGTGGGCGAG 3835
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QY 2641 GCCTGCTTTGGCCTGGTGTGCTGGGCTGGTGTGCTGCTCAGGCTTTCCTGCTGGCTGGC 2700
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QY 2761 TGCTGAGCACACTCTTCTGAGGCGGCGGAGATCTTCTGGAGTCAGAACTGCTCTG 2820

Db 4616 TGCCTGAGCACACTCTTCTGTCAGGGCGCCGAGATCTTCTGTGGAGTCAGAACTGCTCTG 4675
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Db 4676 AGCTGGGCAGACCGGCTGAGTGGCTGCCCTGCGGGGCCCCCTGGGCTGGTGGTCTG 4735
QY 2881 CTGGCCATGTGTGGAGGTGCGACTGTGACCTGGTACCTGGTGGCTTCCCGCCGGAG 2940
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QY 3421 GCTGCTATCCCCCAGCCAGCAGCAATGACCCGCTGTCTCGCTACAGAGACCTTCCCGCTCT 3480
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QY 3481 AGGTTCTGACCCAGGTGTCTCTGACCTGACCCACAGTGAGGCCCTAGGCCCTGGAGC 3540
Db 5336 AGGTTCTGACCCAGGTGTCTCTGACCTGACCCACAGTAAGCCCTAGGCCCTGGAGC 5395
QY 3541 ACGTGGACACCCCTGTGACCATC 3563
Db 5396 ACGTGGACACCCCTGTGACCATC 5418

RESULT 4

ACA62667
ID ACA62667 standard; cDNA; 8001 BP.

XX
AC ACA62667;
XX

DT 19-AUG-2003 (first entry)
XX

DE DNA encoding human calcium sensing G-protein coupled receptor.

XX
KW Human; ds; gene; GPCR; G-protein coupled receptor; gene therapy;
KW parkinson's disease; Huntington's disease; Tourette's syndrome; SNP;
KW single nucleotide polymorphism.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 30. .2588
FT CDS

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US2003036089-A1.

20-FEB-2003.

02-OCT-2002; 2002US-00261482.

20-DEC-1999; 99US-0172600P.

10-OCT-2000; 2000US-00684393.

(APPL-) APPLERA CORP.

Wei M, Zhong W, Ketchum KA, Di Francesco V, Beasley EM;

WPI; 2003-492117/46.

P-PSDB; ABU62106.

New isolated human G-protein coupled receptor proteins, useful for treating e.g. Parkinson's disease, Huntington's disease or Tourette's syndrome, or for developing human therapeutics and diagnostic

PT compositions.
XX Claim 4; Fig 3A-3C; 46pp; English.
PS
XX
CC The invention relates to an isolated human G-protein coupled receptor (GPCR) peptide. The human GPCR peptides and nucleic acid molecules are useful in the development of human therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. Parkinson's disease, Huntington's disease or Tourette's syndrome) characterised by an absence of, inappropriate, or unwanted expression of the GPCR protein, or disorders mediated by proteases. These molecules are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate GPCR activity in cells and tissues that express the GPCR. The peptides are also useful for raising antibodies or eliciting an immune response, as a reagent (including the labelled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids, or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by human proteases. The present sequence represents DNA encoding human calcium sensing G-protein coupled receptor
XX
SQ Sequence 8001 BP; 1291 A; 2632 C; 2623 G; 1455 T; 0 U; 0 Other;

Query Match 95.5%; Score 3403.8; DB 9; Length 8001;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3489; Conservative 0; Mismatches 22; Indels 52; Gaps 2;

QY 1 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGCGCACAACTTTCAGGCCAGGAAGCGA 60
Db |||||
QY 1908 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGCGCACAACTTTCAGGCCAGGAAGCGA 1967
Db |||||
QY 61 GGACACCACACTGGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTCTAAACAAA 120
Db |||||
QY 1968 GGACACCACACTGGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTCTAAACAAA 2027
Db |||||
QY 121 TCCTCTGCCCGTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC 180
Db |||||
QY 2028 TCCTCTGCCCGTCCCGCCCGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC 2087
Db |||||
QY 181 CTGCCGTGCCTGTGGAAGTTGCCTCTGCCATGTGGGGCCCTGTCTCTGGGCTCAGC 240
Db |||||
QY 2088 CTGCCGTGCCTGTGGAAGTTGCCTCTGCCATGTGGGGCCCTGTCTCTGGGCTCAGC 2147
Db |||||
QY 241 CTCTGGGCTCTCCTGCACCCCTGGGACGGGGCCCATTTGTGCCTGTACAGCAACTAGG 300
Db |||||
QY 2148 CTCTGGGCTCTCCTGCACCCCTGGGACGGGGCCCATTTGTGCCTGTACAGCAACTAGG 2207
Db |||||
QY 301 ATGAAGGGGACTACGTCTGGGGGGCTGTTCCTCCCTGGGCGAGGCCGAGGAGGCTGGC 360
Db |||||
QY 2208 ATGAAGGGGACTACGTCTGGGGGGCTGTTCCTCCCTGGGCGAGGCCGAGGAGGCTGGC 2267
Db |||||
QY 361 CTCCGACGCCGACACGGCCCGAGCCCTGTGTGCACCCAGGTACAGAGTGGGACGGCC 420
Db |||||
QY 2268 CTCCGACGCCGACACGGCCCGAGCCCTGTGTGCACCCAGGTACAGAGTGGGACGGCC 2327
Db |||||
QY 421 TGGGTCCGGGTGAGGTGACCCAGGTCTGGGGTCTCCTGAGCTGGGGCCGAGGTGGCCAT 480
Db |||||
QY 2328 TGGGTCCGGGTGAGGTGACCCAGGTCTGGGGTCTCCTGAGCTGGGGCCGAGGTGGCCAT 2387
Db |||||
QY 481 CTGCGGTTCTGTGTGGCCCCAGGTTCTCTCAAACGGCCTGTCTGGGCACTGGCCATGA 540
Db |||||
QY 2388 CTGCGGTTCTGTGTGGCCCCAGGTTCTCTCAAACGGCCTGTCTGGGCACTGGCCATGA 2447
Db |||||
QY 541 AAATGGCCGTGGAGGAGATCAACAAGTCCGATCTGTGCCCGGCTGCGCCTGGGCT 600
Db |||||
QY 2448 AAATGGCCGTGGAGGAGATCAACAAGTCCGATCTGTGCCCGGCTGCGCCTGGGCT 2507
Db |||||
QY 601 ACGACCTCTTTGATACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCAGCCTCATGTTCC 660
Db |||||
QY 2508 ACGACCTCTTTGATACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCAGCCTCATGTTCC 2567
Db |||||

QY	661	TGGCCAAAGCAGGCGAGCCCGGACATCGCCGCTACTGCAACTACACGAGTACCAGCCCC	720
Db	2568	TGGCCAAAGCAGGCGAGCCCGGACATCGCCGCTACTGCAACTACACGAGTACCAGCCCC	2627
QY	721	GTGTGCTGCTGTATCGGGCCCCACTCGTACAGACTCGCCATGGTCAACGGCAAGTTCT	780
Db	2628	GTGTGCTGCTGTATCGGGCCCCACTCGTACAGACTCGCCATGGTCAACGGCAAGTTCT	2687
QY	781	TCAGCTTCTTCTCATGCCCCAGTGGGGCGCCCCACCACCATCACCCACCCCCAACCAACC	840
Db	2688	TCAGCTTCTTCTCATGCCCCAGTGGGGCGCCCCACCACCATCACCCACCCCCAACCAACC	2747
QY	841	CCTGCCCCGTGGAGCCCCCTTGTGTACAGAGATGCTATCATGCACCCCACCGAGCCCTGC	900
Db	2748	CTGCCCGTGGGAG---CCCCGTGTACAGAGATGCCT-----	2781
QY	901	CCTGGGAGCCCTGTGTACAGAGATGCTCTTGGCCTTGCCAGGTACGCTACGGTGTAGCAT	960
Db	2782	-----CTTGGCCCTTGCCAGGTACGCTACGGTGTAGCAT	2815
QY	961	GGAGCTGTAGCGCCCCGGGAGACCTTCCCCCTCCTTCTTCCGCACCGTGCCCCAGGACCG	1020
Db	2816	GGAGCTGTAGCGCCCCGGGAGACCTTCCCCCTCCTTCTTCCGCACCGTGCCCCAGGACCG	2875
QY	1021	TGTGCAGCTGACCGCGCGCGGAGCTGCTGCAGGAGTTCGGCTGGAACCTGGGTGGCCGC	1080
Db	2876	TGTGCAGCTGACCGCGCGCGGAGCTGCTGCAGGAGTTCGGCTGGAACCTGGGTGGCCGC	2935
QY	1081	CCTGGGCAGCGACGACGAGTACGGCCGGCAGGCGCTGAGCATCTTCTCGGCCCTGGCCGC	1140
Db	2936	CCTGGGCAGCGACGACGAGTACGGCCGGCAGGCGCTGAGCATCTTCTCGGCCCTGGCCGC	2995
QY	1141	GGACCGCGGCATCTGCATCGCGCACGAGGGCCTGGTGCCGCTGCCCCCTGCGATGACTC	1200
Db	2996	GGACCGCGGCATCTGCATCGCGCACGAGGGCCTGGTGCCGCTGCCCCCTGCGATGACTC	3055
QY	1201	GGGCTGGGAAGGTGCAGGACGTCTTGACACAGGTGAACACAGACGAGCGTGCAGGTGGT	1260
Db	3056	GGGCTGGGAAGGTGCAGGACGTCTTGACACAGGTGAACACAGACGAGCGTGCAGGTGGT	3115
QY	1261	GCTGCTGTTGCTCCGTGACCGCGCCACCGCCCTCTTCAACTACAGCATCAGCAGCAG	1320
Db	3116	GCTGCTGTTGCTCCGTGACCGCGCCACCGCCCTCTTCAACTACAGCATCAGCAGCAG	3175
QY	1321	GCTTCGCCCCAAGGTGTGGGTGGCCAGCGAGGCCTGGCTGACCTTGACCTGGTCATGGG	1380
Db	3176	GCTTCGCCCCAAGGTGTGGGTGGCCAGCGAGGCCTGGCTGACCTTGACCTGGTCATGGG	3235
QY	1381	GCTGCGCGGCATGGCCCCAGATGGGCACGGTGTGGCTTCTTCCAGAGGGGTGCCAGCT	1440
Db	3236	GCTGCGCGGCATGGCCCCAGATGGGCACGGTGTGGCTTCTTCCAGAGGGGTGCCAGCT	3295
QY	1441	GCACGAGTTCCCCAGTACGTGAAGACGCACCTGGCCCTGGCCACCGACCCCGCCTTCTG	1500
Db	3296	GCACGAGTTCCCCAGTACGTGAAGACGCACCTGGCCCTGGCCACCGACCCCGCCTTCTG	3355
QY	1501	CTCTGCCCTGGCGAGAGGGAGCAGGGTCTGGAGGAGGACGTGGTGGGCCAGCGCTGCC	1560
Db	3356	CTCTGCCCTGGCGAGAGGGAGCAGGGTCTGGAGGAGGACGTGGTGGGCCAGCGCTGCC	3415
QY	1561	GCAGTGTACTGCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCACACACAGACGTT	1620
Db	3416	GCAGTGTACTGCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCACACACAGACGTT	3475
QY	1621	CTCTGTCTACGAGCTGTGTATAGCGTGGCCCCAGGCCCTGCACAAACACTTTCAGTGCAA	1680
Db	3476	CTCTGTCTACGAGCTGTGTATAGCGTGGCCCCAGGCCCTGCACAAACACTTTCAGTGCAA	3535
QY	1681	CGCCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	1740
Db	3536	CGCCTCAGGCTGCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG	3595

Db 4676 AGCTGGGCAGACCGGCTGAGTGGCTGCCTGGGGGCCCTGGGCTGGTGGTGTG 4735
QY 2881 CTGGCCATGCTGGTGGAGGTGCGACTGTGCACCTGGTACCTGGTGGCCCTCCCGCGGAG 2940
Db 4736 CTGGCCATGCTGGTGGAGGTGCGACTGTGCACCTGGTACCTGGTGGCCCTCCCGCGGAG 4795
QY 2941 GTGGTGACGGAAGTGGACATGCTGCCACGGAGGCGCTGGTGCACCTGGCGCACAGCTCC 3000
Db 4796 GTGGTGACGGAAGTGGACATGCTGCCACGGAGGCGCTGGTGCACCTGGCGCACAGCTCC 4855
QY 3001 TGGGTCAGCTTCGGCCCTAGCGCACGCCACCAATGCCAGCTGGCCCTTCTGCTTCCTG 3060
Db 4856 TGGGTCAGCTTCGGCCCTAGCGCACGCCACCAATGCCAGCTGGCCCTTCTGCTTCCTG 4915
QY 3061 GGCACCTTCCTGGTGGGAGCCAGCCGGGCTGCTACAACCGTGCCGCTGGCCTCACCTTT 3120
Db 4916 GGCACCTTCCTGGTGGGAGCCAGCCGGGCGGCTACAACCGTGCCGCTGGCCTCACCTTT 4975
QY 3121 GCCATGCTGGCCCTACTTCATCACCCTGGGTCTCCTTTGTGCCCTCCTGGCCCAATGTGCAG 3180
Db 4976 GCCATGCTGGCCCTACTTCATCACCCTGGGTCTCCTTTGTGCCCTCCTGGCCCAATGTGCAG 5035
QY 3181 GTGTCCTCAGGCCCGCCGCTGCAGATGGGCGCCCTCCTGCTCTGTGCTCTGGGCATCCTG 3240
Db 5036 GTGTCCTCAGGCCCGCCGCTGCAGATGGGCGCCCTCCTGCTCTGTGCTCTGGGCATCCTG 5095
QY 3241 GCTGCTTCACCTGCCAGGTGTACCTGTCTCATGCGGCGAGCCAGGGCTCAACACCCCC 3300
Db 5096 GCTGCTTCACCTGCCAGGTGTACCTGTCTCATGCGGCGAGCCAGGGCTCAACACCCCC 5155
QY 3301 GAGTTCTTCCTGGGAGGGGCCCTGGGGATGCCCAAGGCCAGAAATGACGGGAACACAGGA 3360
Db 5156 GAGTTCTTCCTGGGAGGGGCCCTGGGGATGCCCAAGGCCAGAAATGACGGGAACACAGGA 5215
QY 3361 AATCAGGGGAACATGAGTGACCCAAACCCCTGTGATCTCAGCCCGGTGAACCCAGACTTA 3420
Db 5216 AATCAGGGGAACATGAGTGACCCAAACCCCTGTGATCTCAGCCCGGTGAACCCAGACTTA 5275
QY 3421 GCTGCGATCCCCCAGCCAGCAATGACCCGCTGTCTCGCTACAGAGACCCCTCCCGCTCT 3480
Db 5276 GCTGCGATCCCCCAGCCAGCAATGACCCGCTGTCTCGCTACAGAGACCCCTCCCGCTCT 5335
QY 3481 AGGTTCTGACCCCGAGTTGTCTCCTGACCCTGACCCCAAGTACAGCCCTAGGCTTGAGC 3540
Db 5336 AGGTTCTGACCCCGAGTTGTCTCCTGACCCTGACCCCAAGTACAGCCCTAGGCTTGAGC 5395
QY 3541 ACGTGGACACCCCTGTGACCATC 3563
Db 5396 ACGTGGACACCCCTGTGACCATC 5418

RESULT 5
ADC86148
ID ADC86148 standard; DNA; 4256 BP.
XX
AC ADC86148;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:601.
XX
KW ds; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.

PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI; 2003-315783/31.
DR P-PSDB; ADC86149.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 1; SEQ ID NO 601; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
SQ Sequence 4256 BP; 707 A; 1445 C; 1370 G; 734 T; 0 U; 0 Other;
Query Match 95.4%; Score 3398.6; DB 10; Length 4256;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 3482; Conservative 0; Mismatches 19; Indels 52; Gaps 2;
QY 11 TGGCCTCAGGCAGAGTCTGACGCGCACAAACTTTTCAGGCCCGAGGAGGACACCACT 70
Db 1 TGGCCTCAGGCAGAGTCTGACGCGCACAAACTTTTCAGGCCCGAGGAGGACACCACT 60
QY 71 GGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTAAACAAATCCTCTGCCC 130
Db 61 GGGGCCCCAGGGTGTGGCAAGTGAGGATGGCAAGGTTTGTAAACAAATCCTCTGCCC 120
QY 131 GCTCCCCCGCCCGGCTCACTCCATGTAGGCCCCAGTGGGGCAGCCACCTGCCGTGCC 190
Db 121 GCTCCCCCGCCCGGCTCACTCCATGTAGGCCCCAGTGGGGCAGCCACCTGCCGTGCC 180
QY 191 TGTGGAAGTTGCCCTCTGCCATGTGGGCCCTGTCTGTCTGGCCCTCAGCCCTCTGGGCTC 250
Db 181 TGTGGAAGTTGCCCTCTGCCATGTGGGCCCTGTCTGTCTGGCCCTCAGCCCTCTGGGCTC 240
QY 251 TCCTGCACCCCTGGGACGGGGCCCCCATTTGTGCCCTGTACAGCAACTTAGGATGAAGGGG 310
Db 241 TCCTGCACCCCTGGGACGGGGCCCCCATTTGTGCCCTGTACAGCAACTTAGGATGAAGGGG 300
QY 311 ACTACGTGCTGGGGGGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGAGCC 370
Db 301 ACTACGTGCTGGGGGGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGAGCC 360
QY 371 GGACACGGCCCCAGAGCCCTGTGTGCACCAAGGTACAGAGGTGGGACGGCCTGGGTGCGGG 430
Db 361 GGACACGGCCCCAGAGCCCTGTGTGCACCAAGGTACAGAGGTGGGACGGCCTGGGTGCGGG 420
QY 431 TCAGGGTGACCAAGTCTGGGGTGTCTCCTGAGCTGGGGCCGAGGTGGCCATCTCGGTTCT 490
Db 421 TCAGGGTGACCAAGTCTGGGGTGTCTCCTGAGCTGGGGCCGAGGTGGCCATCTCGGTTCT 480
QY 491 GTGTGGCCCCAGGTTCTCCTCAAACGGCCCTGTCTTGGGCACCTGGCCATGAAAATGGCCGT 550
Db 481 GTGTGGCCCCAGGTTCTCCTCAAACGGCCCTGTCTTGGGCACCTGGCCATGAAAATGGCCGT 540
QY 551 GGAGGAGATCAACAAGTCGGATCTGCTGCCCGGGCTGGCCCTGGGCTACGACCTCTT 610
Db 541 GGAGGAGATCAACAAGTCGGATCTGCTGCCCGGGCTGGCCCTGGGCTACGACCTCTT 600
QY 611 TGATACGTGCTGGAGCCCTGTGGTGCCATGAAGCCCGAGCCTCATGTTCTTGCCCAAGGC 670

Db 601 TGATACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCAGCCTCATGTTCTTGSCAAAGGC 660
QY 671 AGGCAGCCGCGACATCGCGCCTACTGCAACTACAGCAGTACCAGCCCGCTGCTGGC 730
Db 661 AGGCAGCCGCGACATCGCGCCTACTGCAACTACAGCAGTACCAGCCCGCTGCTGGC 720
QY 731 TGTATCGGGCCCCACTCGTCAGAGCTCGCCATGGTACCGGCAAGTTCTTCAGCTTCTT 790
Db 721 TGTATCGGGCCCCACTCGTCAGAGCTCGCCATGGTACCGGCAAGTTCTTCAGCTTCTT 780
QY 791 CCTATGCCCCAGTGGGGGCCCCCACCACCATCACCCACCCCCAACCAACCCCTGCCCGT 850
Db 781 CCTATGCCCCAGTGGGGGCCCCCACCACCATCACCCACCCCCAACCAACCCCTGCCCGTGG 840
QY 851 GGGAGCCCTTGTGTAGGAGAAATGCTACATGCAACCCACCCAGCCCTGCCCTGGGAGCC 910
Db 841 GAG--CCCCTGTGTAGGAGATGCTT----- 864
QY 911 CTGTGTCAAGATGCTTGTGGCTTGCAGGTACGCTACGGTGTAGCATGGAGTGTCTG 970
Db 865 -----CTTGGCCCTTGACGGTACGCTACGGTGTAGCATGGAGTGTCTG 908
QY 971 AGGCCCCGGAGACCTTCCCCTCTTCTCCGACCGTGCCAGCGACCGTGTGACGCTG 1030
Db 909 AGGCCCCGGAGACCTTCCCCTCTTCTCCGACCGTGCCAGCGACCGTGTGACGCTG 968
QY 1031 ACGGCCGCGGAGCTGCTGACGAGTTCGGCTGGAACCTGGTGGCCCGCTGGCGAGC 1090
Db 969 ACGGCCGCGGAGCTGCTGACGAGTTCGGCTGGAACCTGGTGGCCCGCTGGCGAGC 1028
QY 1091 GACGACGAGTACGGCCGGCAGGCGCTGAGCATCTTCTCGGCCCTGGCCGCGCAGCGGC 1150
Db 1029 GACGACGAGTACGGCCGGCAGGCGCTGAGCATCTTCTCGGCCCTGGCCGCGCAGCGGC 1088
QY 1151 ATCTGATCGCGCACAGGGCCTGGTGGCCTGCCCCGTGCCGATGACTCGCGCTGGG 1210
Db 1089 ATCTGATCGCGCACAGGGCCTGGTGGCCTGCCCCGTGCCGATGACTCGCGCTGGG 1148
QY 1211 AAGGTGACGAGCCTCTGACACAGGTGAACAGAGCAGCGTGCAGTGGTGTCTGTTT 1270
Db 1149 AAGGTGACGAGCCTCTGACACAGGTGAACAGAGCAGCGTGCAGTGGTGTCTGTTT 1208
QY 1271 GCCTCCGTGACCGCCGCCACGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCC 1330
Db 1209 GCCTCCGTGACCGCCGCCACGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCC 1268
QY 1331 AAGGTGTTGGTGGCCAGCGAGGCTGGCTGACCTTGAACCTGCTCATGGGCTGCCCGGC 1390
Db 1269 AAGGTGTTGGTGGCCAGCGAGGCTGGCTGACCTTGAACCTGCTCATGGGCTGCCCGGC 1328
QY 1391 ATGGCCAGATGGGCACGGTGTCTGGCTTCCAGAGGGGTGCCAGTGCACGAGTTC 1450
Db 1329 ATGGCCAGATGGGCACGGTGTCTGGCTTCCAGAGGGGTGCCAGTGCACGAGTTC 1388
QY 1451 CCCAGTACGTGAAGACGACCTGGCCCTGGCCACCGACCCCGCCTTCTGCTTGCCTG 1510
Db 1389 CCCAGTACGTGAAGACGACCTGGCCCTGGCCACCGACCCCGCCTTCTGCTTGCCTG 1448
QY 1511 GCGAGAGGAGCAGGCTTGGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGAC 1570
Db 1449 GCGAGAGGAGCAGGCTTGGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGAC 1508
QY 1571 TGATACGCTGCAGAACGTGAGCGCAGGGCTAAATCACACAGACGTTCTGTGTAC 1630
Db 1509 TGATACGCTGCAGAACGTGAGCGCAGGGCTAAATCACACAGACGTTCTGTGTAC 1568
QY 1631 GCAGCTGTATAGCTGSCCAGGCCCTGCACAACTCTTCACTGCAACGCTCAGGC 1690
Db 1569 GCAGCTGTATAGCTGSCCAGGCCCTGCACAACTCTTCACTGCAACGCTCAGGC 1628
QY 1691 TGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGGGGTGTGCTG 1750
Db 1629 TGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGGGGTGTGCTG 1688

QY 1751 TCCTCTGCAATGTGCCAGGCCACACAGGCACGGCCACCGCCTGAGCTGAGGTGGCTGG 1810
Db 1689 TCCTCTGCAATGTGCCAGGCCACACAGGCACGGCCACCGCCTGAGCTGAGGTGGCTGG 1748
QY 1811 CGGCTCAGCCCGCTCCCGCCCGCCGAGCTCCTGGAGAACATGTACAACTGACTTCCAC 1870
Db 1749 CGGCTCAGCCCGCTCCCGCCCGCCGAGCTCCTGGAGAACATGTACAACTGACTTCCAC 1808
QY 1871 GTGGCGGGCTGCCGCTGCGGTTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACTG 1930
Db 1809 GTGGCGGGCTGCCGCTGCGGTTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACTG 1868
QY 1931 AAGCTGTGGGTGTGGCAGGGCTCAGTGCCCCAGGCTCCACGACGTGGGCAGGTTCAACGC 1990
Db 1869 AAGCTGTGGGTGTGGCAGGGCTCAGTGCCCCAGGCTCCACGACGTGGGCAGGTTCAACGC 1928
QY 1991 AGCCTCAGGACAGAGCGCTGAAGATCCGCTGGCACACGCTGTGACAAACAGGTGAGTGA 2050
Db 1929 AGCCTCAGGACAGAGCGCTGAAGATCCGCTGGCACACGCTGTGACAAACAGGTGAGTGA 1988
QY 2051 GGGTGGGTGTGCCAGGCTGCCCGTGGTGTAGCCCCCGGCGAGGGCGCAGCCTGGGGTGG 2110
Db 1989 GGGTGGGTGTGCCAGGCTGCCCGTGGTGTAGCCCCCGGCGAGGGCGCAGCCTGGGGTGG 2048
QY 2111 GGGCGGTTCCAGTCTCCCGTGGCATGCCAGCCGAGCAGAGCCAGACCCAGGCCTGTG 2170
Db 2049 GGGCGGTTCCAGTCTCCCGTGGCATGCCAGCCGAGCAGAGCCAGAGCCAGAGCCAGGCCTGTG 2108
QY 2171 CGCAGAACCCCGTGTCCCGGTGTCCGGCAGTGCCAGGAGGGCCAGGTGCGCCGGTCA 2230
Db 2109 CGCAGAACCCCGTGTCCCGGTGTCCGGCAGTGCCAGGAGGGCCAGGTGCGCCGGTCA 2168
QY 2231 AGGGTTCACCTCCTGCTGCTACGACTGTGTGACTGCGAGCGGGCAGCTACCGGCAAA 2290
Db 2169 AGGGTTCACCTCCTGCTGCTACGACTGTGTGACTGCGAGCGGGCAGCTACCGGCAAA 2228
QY 2291 ACCAGGTGAGCCGCTTCCCGCAGCGCGGGTGGAAACGACAGAGGGGAGGTCTCTGC 2350
Db 2229 ACCAGGTGAGCCGCTTCCCGCAGCGCGGGTGGAAACGACAGAGGGGAGGTCTCTGC 2288
QY 2351 CAAGTCTGACTCTGAGAACAGAGCCACAGGGTACAAGACGAAACACCCAGCCCTTCT 2410
Db 2289 CAAGTCTGACTCTGAGAACAGAGCCACAGGGTACAAGACGAAACACCCAGCCCTTCT 2348
QY 2411 CCTCTCTCACAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGC 2470
Db 2349 CCTCTCTCACAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGC 2408
QY 2471 GAAGCACACGCTGCTTCCCGCCGACGCTCGGTTCTTGCCATGGGCGAGCCGGTGTGC 2530
Db 2409 GAAGCACACGCTGCTTCCCGCCGACGCTCGGTTCTTGCCATGGGCGAGCCGGTGTGC 2468
QY 2531 TGCTGCTGCTCTGCTGAGCCCTGGGCTGGGCTTGTGTGCTGGTGGTGGGCTGT 2590
Db 2469 TGCTGCTGCTCTGCTGAGCCCTGGGCTGGGCTTGTGTGCTGGTGGTGGGCTGT 2528
QY 2591 TCGTTACCATCGGACAGCCCACTGGTTTCAGGCTCGGGGGGGCCCTTGGCCTGCTTTG 2650
Db 2529 TCGTTACCATCGGACAGCCCACTGGTTTCAGGCTCGGGGGGGCCCTTGGCCTGCTTTG 2588
QY 2651 GCCTGCTGCTGGGCTGGTCTGGTCTGGCTCCTCCTGTTCCCTGCGCAGCCAGCCAGCC 2710
Db 2589 GCCTGCTGCTGGGCTGGTCTGGTCTGGCTCCTCCTGTTCCCTGCGCAGCCAGCCAGCC 2648
QY 2711 CTGCCCCGATGCTGGCCAGCAGCCCTTGTCCACCTCCCGCTACGGGCTGCTGAGCA 2770
Db 2649 CTGCCCCGATGCTGGCCAGCAGCCCTTGTCCACCTCCCGCTACGGGCTGCTGAGCA 2708
QY 2771 CACTCTTCTGCGAGCGCCGAGATCTTCTGTTGAGTCAAGAACTGCCTCTGAGCTGGCAG 2830
Db 2709 CACTCTTCTGCGAGCGCCGAGATCTTCTGTTGAGTCAAGAACTGCCTCTGAGCTGGCAG 2768

QY 2831 ACCGGCTGAGTGGCTGCCTCGGGGGCCCTGGGCCTGGCTGGTGGTGGCTGGCCATGC 2890
Db |||||
QY 2769 ACCGGCTGAGTGGCTGCCTCGGGGGCCCTGGGCCTGGCTGGTGGTGGCTGGCCATGC 2828
Db |||||
QY 2891 TGGTGGAGTGCACACTGTGCACCTGTGTACCTGGTGGCTTCCCGCGAGGTGGTGACGG 2950
Db |||||
QY 2829 TGGTGGAGTGCACACTGTGCACCTGTGTACCTGGTGGCTTCCCGCGAGGTGGTGACGG 2888
QY 2951 ACTGGACATGCTGCCACCGGAGGCGTGTGCACTGCCGCACACGCTCCTGGGTGAGCT 3010
Db |||||
QY 2889 ACTGGACATGCTGCCACCGGAGGCGTGTGCACTGCCGCACACGCTCCTGGGTGAGCT 2948
QY 3011 TCGGCTGAGCGCACGCCACCAATGCCACGCTGGCCTTCTCTGCTTCTCTGGCACTTTCC 3070
Db |||||
QY 2949 TCGGCTGAGCGCACGCCACCAATGCCACGCTGGCCTTCTCTGCTTCTCTGGCACTTTCC 3008
QY 3071 TGGTGGAGCCAGCCCGGGCTGCTACAACCGTGGCCGCTCACCTTTGCCATGCTGG 3130
Db |||||
QY 3009 TGGTGGAGCCAGCCCGGGCTGCTACAACCGTGGCCGCTCACCTTTGCCATGCTGG 3068
QY 3131 CCTACTTCATCACCTGGGTCTCTTTGTGCCCTCCTGGCCAAATGTGCAGGTGGTCTCA 3190
Db |||||
QY 3069 CCTACTTCATCACCTGGGTCTCTTTGTGCCCTCCTGGCCAAATGTGCAGGTGGTCTCA 3128
QY 3191 GGCCCGCGTGCAGATGGCGGCTCCTGCTGTGTGCTTCTGGCATCCTGGCTGCTTCC 3250
Db |||||
QY 3129 GGCCCGCGTGCAGATGGCGGCTCCTGCTGTGTGCTTCTGGCATCCTGGCTGCTTCC 3188
QY 3251 ACCTGCCAGGTGTTACCTGCTCATGCGGCGCAGCCAGGGCTCAACACCCCGAGTTCTTCC 3310
Db |||||
QY 3189 ACCTGCCAGGTGTTACCTGCTCATGCGGCGCAGCCAGGGCTCAACACCCCGAGTTCTTCC 3248
QY 3311 TGGGAGGGGCGCCCTGGGGATGCCAAGGCCAGCAATGACGGGAACACAGGAAATCAGGGGA 3370
Db |||||
QY 3249 TGGGAGGGGCGCCCTGGGGATGCCAAGGCCAGCAATGACGGGAACACAGGAAATCAGGGGA 3308
QY 3371 AACATGAGTGACCCCAACCTGTGATCTCAGCCCCGGTGAAACCCAGACTTAGCTGGCATCC 3430
Db |||||
QY 3309 AACATGAGTGACCCCAACCTGTGATCTCAGCCCCGGTGAAACCCAGACTTAGCTGGCATCC 3368
QY 3431 CCCCCAAGCCAGCAATGACCCCGTGTCTCGTACAGAGACCCTCCCGCTCTAGGTTCTGAC 3490
Db |||||
QY 3369 CCCCCAAGCCAGCAATGACCCCGTGTCTCGTACAGAGACCCTCCCGCTCTAGGTTCTGAC 3428
QY 3491 CCCAGTTGTCTCTGACCCCTGACCCCAAGCCAGTACGCTAGCCCTAGGCTGGAGCACGTTGGACAC 3550
Db |||||
QY 3429 CCCAGTTGTCTCTGACCCCTGACCCCAAGCCAGTACGCTAGCCCTAGGCTGGAGCACGTTGGACAC 3488
QY 3551 CCCTGTGACCATC 3563
Db |||||
QY 3489 CCCTGTGACCATC 3501

RESULT 6
ID ADK90723
XX ADK90723 standard; DNA; 3200 BP.
AC ADK90723;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Human taste receptor Tlr3 genomic sequence.
XX
KW gene therapy; taste receptor; Tlr3; Tlr1; Tlr2; taste-induced behavior;
KW taste topographic map; tongue; taste cell; taste sensory neuron;
XX brain taste center; gene; ds.
OS Homo sapiens.
XX
PN WO2003004992-A2.
XX
PD 16-JAN-2003.
XX

PF 03-JUL-2002; 2002WO-US021269.
XX
PR 03-JUL-2001; 2001US-0302898P.
PR 10-AUG-2001; 2001US-00927315.
PR 22-FEB-2002; 2002US-0358925P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Zuker CS, Ryba NJP, Chandrashekar J, Hoon MA, Nelson GA, Zhang Y;
XX
DR WPI; 2003-210382/20.
XX
PT New taste receptors comprising a Tlr3 polypeptide and optionally a Tlr1
PT or Tlr2 polypeptide, useful as probes for identifying taste cells, and in
PT gene therapy for correcting acquired and inherited genetic defects.
XX
PS Disclosure; SEQ ID NO 13; 119pp; English.
XX
CC The invention relates to a novel taste receptor comprising a Tlr3
CC polypeptide and optionally a Tlr1 or Tlr2 polypeptide. The nucleic acids
CC and proteins encoding the receptors may be used as probes to identify
CC taste cells or subsets of taste cells or to dissect taste-induced
CC behaviors, and in the generation of taste topographic maps that elucidate
CC the relationship between the taste cells of the tongue and taste sensory
CC neurons leading to taste centers in the brain. Nucleic acids encoding Tlr
CC protein can be used with highly density oligonucleotide array technology
CC to identify Tlr protein, orthologs, alleles, conservatively modified
CC variants, and polymorphic variants in this invention. The nucleic acids
CC may be inserted into vectors for gene therapy correct acquired and
CC inherited genetic defects and other diseases. Compositions may be
CC administered to elicit a therapeutic response in the patient. Modulators
CC of sweet and/or amino acid taste transduction are useful for
CC pharmacological and genetic modulation of sweet and amino acid taste
CC ligands, and in food and pharmaceutical industries to customize taste.
CC This sequence corresponds to the genomic DNA encoding the human Tlr3
CC protein.
XX
SQ Sequence 3200 BP; 469 A; 1083 C; 1070 G; 578 T; 0 U; 0 Other;

Query Match 86.7%; Score 3088.2; DB 10; Length 3200;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3182; Conservative 0; Mismatches 18; Indels 53; Gaps 3;
QY 145 GCTCACTCCATGTAGGCCCCCAGTCGGGGCAGCCACCTGCCGTGCTTGGAGTTGCC 204
Db |||||
1 GCTCACTCCATGTAGGCCCCCAGTCGGGGCAGCCACCTGCCGTGCTTGGAGTTGCC 60
QY 205 TCTGCCATGTGGGCCCTGCTGTCTTGGCCCTCAGCCCTCTGGCTCTCCTGCACCCCTGGG 264
Db |||||
61 TCTGCCATGTGGGCCCTGCTGTCTTGGCCCTCAGCCCTCTGGCTCTCCTGCACCCCTGGG 120
QY 265 ACGGGGCCCCCATGTGCTGTCTCACAGCACTTAGGATGAAGGGGACTACCTGCTGGGG 324
Db |||||
121 ACGGGGCCCCCATGTGCTGTCTCACAGCACTTAGGATGAAGGGGACTACCTGCTGGGG 180
QY 325 GGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCCTCCGACGCCGACACGCCCCAGC 384
Db |||||
181 GGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCCTCCGACGCCGACACGCCCCAGC 240
QY 385 AGCCCTGTGTGACACAGGTACAGAGTGGGACGGCCCTGGGTCCGGGTGAGGGTGACCCAGG 444
Db |||||
241 AGCCCTGTGTGACACAGGTACAGAGTGGGACGGCCCTGGGTCCGGGTGAGGGTGACCCAGG 300
QY 445 TCTGGGTGCTCCTGAGCTGGGCGCAGGTGGCCATCTGCGGTCTCTGTGTGGCCCCAGGT 504
Db |||||
301 TCTGGGTGCTCCTGAGCTGGGCGCAGGTGGCCATCTGCGGTCTCTGTGTGGCCCCAGGT 360
QY 505 TCTCCTCAAAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCCCTGGAGGAGATCAACA 564
Db |||||
361 TCTCCTCAAAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCCCTGGAGGAGATCAACA 420
QY 565 ACAAGTCGATCTGTGCCCGGGCTGCGCCCTGGGCTACGACCTCTTTGATACGTGCTCGG 624

Db 301 CAAACGGCCTGCTCTGGGCACCTGGCCATGAAATGGCCGTGGAGGAGATCAACAAACAAGT 360

QY 571 CGGATCTGCTGCCCGGCTGCGCTGGGCTACGACCTCTTTGATACGTGCTGGAGCCTG 630

Db 361 CGGATCTGCTGCCCGGCTGCGCTGGGCTACGACCTCTTTGATACGTGCTGGAGCCTG 420

QY 631 TGGTGGCCATGAAGCCAGCCCTCATGTTCTCTGGCCAAAGGCAGGCAGCCCGACATCGCCG 690

Db 421 TGGTGGCCATGAAGCCAGCCCTCATGTTCTCTGGCCAAAGGCAGGCAGCCCGACATCGCCG 480

QY 691 CCTACTGCAACTACACGAGTACCAGCCCGCTGCTGGCTGTCTATCGGGCCCGCACTCGT 750

Db 481 CCTACTGCAACTACACGAGTACCAGCCCGCTGCTGGCTGTCTATCGGGCCCGCACTCGT 540

QY 751 CAGAGCTCGCCATGGTCAACGGCAAGTTCTTACGCTTCTTCCCTCATGCCCGAGTGGGGCG 810

Db 541 CAGAGCTCGCCATGGTCAACGGCAAGTTCTTACGCTTCTTCCCTCATGCCCGAG-GTGGCG 599

QY 811 CCCCCCACCATACCCACCCCGCAACCCCTGCCCCGTGGAGCCCCCTTGTGTACAGGA 870

Db 600 CCCCCCACCATACCCACCCCGCAACCCCTGCCCCGTGGAG---CCCCGTGTACAGGA 656

QY 871 GAATGCTACATGCACCCACCCAGCCCTGCCCTGGGAGCCCTGTGTCAAGAAGATGCTCTT 930

Db 657 GATGCCT-----CTTG 667

QY 931 GGCCCTGCAGGTACGCTACGGTGTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCC 990

Db 668 GCCCTGCAGGTACGCTACGGTGTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCC 727

QY 991 CTCCTTCTTCGGCACCGTGCACGGACCGTGTGCAGCTGACGGCCCGCCGGAGCTGCT 1050

Db 728 CTCCTTCTTCGGCACCGTGCACGGACCGTGTGCAGCTGACGGCCCGCCGGAGCTGCT 787

QY 1051 GCAGGAGTTGGCTGGAACCTGGGTGGCCGCCCTGGGACGACGAGTACGGCCCGGCA 1110

Db 788 GCAGGAGTTGGCTGGAACCTGGGTGGCCGCCCTGGGACGACGAGTACGGCCCGGCA 847

QY 1111 GGGCTGAGCATCTTCTCGGCCCTGGCCCGCGGACCGGGCATCTGCATCGCGCACGAGG 1170

Db 848 GGGCTGAGCATCTTCTCGGCCCTGG-CTCGGCACCGGCACTGTCATCGCGCACGAGG 906

QY 1171 CTTGTGCGCTGCCCGCTGCCGATGACTCGGGCTGGGAAGGTGCAGGACGTCTTGCA 1230

Db 907 CTTGTGCGCTGCCCGCTGCCGATGACTCGGGCTGGGAAGGTGCAGGACGTCTTGCA 966

QY 1231 CCAGGTGAACACAGAGCAGCGTGCAGTGGTGTCTGTTTCGCTCCGTGCACGCCGCCCA 1290

Db 967 CCAGGTGAACACAGAGCAGCGTGCAGTGGTGTCTGTTTCGCTCCGTGCACGCCGCCCA 1026

QY 1291 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGTGTGGTGGCCAGCGA 1350

Db 1027 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGTGTGGTGGCCAGCGA 1086

QY 1351 GGCCTGGCTGACCTCTGACCTGGTCAATGGGGCTGCCCGGCATGGCCCCAGATGGGCACCGT 1410

Db 1087 GGCCTGGCTGACCTCTGACCTGGTCAATGGGGCTGCCCGGCATGGCCCCAGATGGGCACCGT 1146

QY 1411 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACGAGTTCCCCAGTACGTGAAGACGCA 1470

Db 1147 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACGAGTTCCCCAGTACGTGAAGACGCA 1206

QY 1471 CCTGGCCCTGGCCACCGACCCCGCCTTCTGCTCTGCCCTGGCGAGAGGGAGCAGGGTCT 1530

Db 1207 CCTGGCCCTGGCCACCGACCCCGCCTTCTGCTCTGCCCTGGCGAGAGGGAGCAGGGTCT 1266

QY 1531 GGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGACTGCATCAGCTGCAGAACGT 1590

Db 1267 GGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGACTGCATCAGCTGCAGAACGT 1326

QY 1591 GAGCGCAGGGCTAAATCACCACAGACGTTCTGTCTACGCAGCTGTGTATAGCGTGGC 1650

Db 1327 GAGCGCAGGGCTAAATCACCACAGACGTTCTGTCTACGCAGCTGTGTATAGCGT-GC 1385

QY 1651 CCAGGCCCTGCACAAACACTCTTTAGTGCACGCTCAGGCTGCCCCGCGAGGACCCCGT 1710

Db 1386 CCAGGCCCTGCACAAACACTCTTTAGTGCACGCTCAGGCTGCCCCGCGAGGACCCCGT 1445

QY 1711 GAAGCCCTGGCAGGTGAGCCCGGAGATGGGGGTGTGTCTCTCTCATGTGCGCCAGGC 1770

Db 1446 GAAGCCCTGGCAGGTGAGCCCGGAGATGGGGGTGTGTCTCTCTCATGTGCGCCAGGC 1505

QY 1771 CACCAGGCA CGGCCACACCGCCTGAGCTGGAGGTGGCTGGCGCTCAGCCCCCTCCCCCG 1830

Db 1506 CACCAGGCA CGGCCACACCGCCTGAGCTGGAGGTGGCTGGCGCTCAGCCCCCTCCCCCG 1565

QY 1831 CCCGCAGCTCCTGAGAAACATGTACAACCTGACCTTCCACGTGGCGGGGCTGCCGTGCG 1890

Db 1566 CCCGCAGCTCCTGGAGAAACATGTACAACCTGACCTTCCACGTGGCGGGGCTGCCGTGCG 1625

QY 1891 GTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1950

Db 1626 GTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1685

QY 1951 CTCAGTGCCCGAGGCTCCACGACGTGGGAGGTTCAACGGCAGCCTCAGGACAGAGCGCT 2010

Db 1686 CTCAGTGCCCGAGGCTCCACGACGTGGGAGGTTCAACGGCAGCCTCAGGACAGAGCGCT 1745

QY 2011 GAAGATCCGCTGGCACACGTCTGACAAACAGGTGAGGTGAGGTGGGTGTGCCAGGGCTG 2070

Db 1746 GAAGATCCGCTGGCACACGTCTGACAAACAGGTGAGGTGAGGTGGGTGTGCCAGGGCTG 1805

QY 2071 CCCGTGGTAGCCCCCGCGCAGGGCGCAGCCTTGGGGGTGGGGCCGTTCCAGTCTCCCGT 2130

Db 1806 CCCGTGGTAGCCCCCGCGCAGGGCGCAGCCTTGGGGGTGGGGCCGTTCCAGTCTCCCGT 1865

QY 2131 GGGCATGCCCAGCCGAGAGAGCCAGACCCCGAGCCTGTGTGCGCAGAAAGCCCGTGTCCCGG 2190

Db 1866 -GGCATGCCCAGCCGAGAGAGCCAGACCCCGAGCCTGTGTGCGCAGAAAGCCCGTGTCCCGG 1924

QY 2191 TGCTCGCGGAGTGCCAGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGC 2250

Db 1925 TGCTCGCGGAGTGCCAGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGC 1984

QY 2251 TAGCACTGTGTGACTGCGAGGCGGGCAGCTACCGGCAAAACCCAGGTGAGCCGCTTCC 2310

Db 1985 TAGCACTGTGTGACTGCGAGGCGGGCAGCTACCGGCAAAACCCAGGTGAGCCGCTTCC 2044

QY 2311 CGCAGGCGGGGGTGGAAACGACAGAGGGAGGGTCTTGCAAGTCTGACTCTGAGACC 2370

Db 2045 CGCAGGCGGGGGTGGAAACGACAGAGGGAGGGTCTTGCAAGTCTGACTCTGAGACC 2104

QY 2371 AGAGCCACAGGGTACAAGACGAACACCCAGCGCCCTTCTCTCTCTCACAGACGACATC 2430

Db 2105 AGAGCCACAGGGGACAAGACGAACACCCAGCGCCCTTCTCTCTCTCACAGACGACATC 2164

QY 2431 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCCCGGAGCGAAGCACACGCTTCCGC 2490

Db 2165 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCCCGGAGCGAAGCACACGCTTCCGC 2224

QY 2491 CGAGGTCTCGGTTCTTGCAATGGGGCGAGCCGGCTGTGTGCTGCTGCTCCTGCTGCTG 2550

Db 2225 CGCAGGTCTCGGTTCTTGCAATGGGGCGAGCCGGCTGTGTGCTGCTGCTCCTGCTGCTG 2284

QY 2551 AGCCTGGCGCTGGGCTTGTGCTGGCTGCTTTGGGGCTGTTCGTTACCATCGGACAGC 2610

Db 2285 AGCCTGGCGCTGGGCTTGTGCTGGCTGCTTTGGGGCTGTTCGTTACCATCGGACAGC 2344

QY 2611 CCACGTGTTCAGGCTCGGGGGGCCCCCTGGCCTGCTTTGGCCTGCTGCTGCTGGCCTG 2670

Db 2345 CCACGTGTTCAGGCTCGGGGGGCCCCCTGGCCTGCTTTGGCCTGCTGCTGCTGGCCTG 2404

QY 2671 GTCTGCTCAGCGTCTCTCCTGTTCCCTGGCCAGCCCCAGCCCTGCCCGATGCTGGCCAG 2730

Db 2405 GTCTGCTCAGCGTCTCTCCTGTTCCCTGGCCAGCCCCAGCCCTGCCCGATGCTGGCCAG 2464

Db 2281 GTGCCCCCTCTGGCCAAATGTGCAGGTGGTCTCAGGCCCGCGCGTGCAGATGGCGCCCTC 2340
QY 3217 CTGCTCTGTGCTCTGGGCATCCTGGTGCCTTCCACCTGCCAGGTGTACCTGCTCATG 3276
Db 2341 CTGCTCTGTGCTCTGGGCATCCTGGTGCCTTCCACCTGCCAGGTGTACCTGCTCATG 2400
QY 3277 CGGCAGCCAGGGCTCAACACCCCCGAGTTCTTCTGGGAGGGGGCCCTGGGGATGCCCAA 3336
Db 2401 CGGCAGCCAGGGCTCAACACCCCCGAGTTCTTCTGGGAGGGGGCCCTGGGGATGCCCAA 2460
QY 3337 GGCAGGAATGACGGGAACACAGGAATCAGGGGAAACATGAGTGACCCAACTCTGTGATC 3396
Db 2461 GGCAGGAATGACGGGAACACAGGAATCAGGGGAAACATGAGTGACCCAACTCTGTGATC 2520
QY 3397 TCAGCCCCGGTGAACCCAGACTTAGCTGGGATCCCCCAGGTTGTCTCTGACCCCTGACCC 3456
Db 2521 TCAGCCCCGGTGAACCCAGACTTAGCTGGGATCCCCCAGGTTGTCTCTGACCCCTGACCC 2580
QY 3457 TCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCCGAGTTGTCTCTGACCCCTGACCC 3516
Db 2581 TCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCCGAGTTGTCTCTGACCCCTGACCC 2640
QY 3517 CACAGTGAGCCCTAGGCTGGAGCAGCTGGACCCCTGTGACCATC 3563
Db 2641 CACAGTGAGCCCTAGGCTGGAGCAGCTGGACCCCTGTGACCATC 2687

RESULT 9
ADI40945
ID ADI40945 standard; cDNA; 2685 BP.
XX
AC ADI40945;
XX
DT 22-APR-2004 (first entry)
XX
DE Human G protein-coupled receptor HGPRBMY30_3 cDNA.

XX Human; ss; gene; GPCR; G protein-coupled receptor; reproductive disorder;
KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;
KW XX male; epididymitis; cryptorchidism; sperm transport disorder;
KW testicular cancer; testicular germ cell tumour; male hormone disorder;
KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;
KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;
KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;
KW graft-versus-host disease; autoimmunity disorder;
KW systemic lupus erythematosus; drug induced haemolytic anaemia;
KW Sjogren's disease; T-cell maturation disorder;
KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;
KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;
KW pulmonary disorder; brain disorder; endocrine disorder; cancer;
XX gene therapy.

OS Homo sapiens.
XX
PN US2004018976-A1.
XX
PD 29-JAN-2004.
XX
PF 13-MAY-2003; 2003US-00436715.
XX
PR 14-MAY-2002; 2002US-0380336P.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
XX
PI Feder JN, Mintier G, Ramanathan CS;
XX
DR WPI; 2004-122081/12.
DR P-PSDB; ADI40946.
XX
PT New human G-protein coupled receptor polypeptide and polynucleotide,

PT useful for diagnosing, preventing, treating or ameliorating a medical
PT condition, e.g. reproductive disorder, immunodeficiency disease or
PT testicular cancer.
XX
PS
XX Claim 1; SEQ ID NO 5; 290pp; English.

CC The invention relates to an isolated human G protein-coupled receptor
CC polypeptide and its encoding polynucleotide, including the full length
CC proteins minus the start methionine (and the region of the polynucleotide
CC encoding this protein region). The proteins are designated HGPRBMY30-1,
CC HGPRBMY30-2, HGPRBMY30-3, HGPRBMY41-1, HGPRBMY41-2, HGPRBMY41-3,
CC HGPRBMY42, HGPRBMY42-1, HGPRBMY43 and HGPRBMY44. Also included are
CC expression vectors, host cells, antibodies, preventing (treating or
CC ameliorating) a medical condition comprising administering to a mammalian
CC subject the polypeptide or its modulator and diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject
CC (comprising determining the presence or absence of a mutation in the
CC polynucleotide, or the presence or amount of expression of the
CC polypeptide in a biological sample and diagnosing a pathological
CC condition or a susceptibility to a pathological condition based on the
CC presence or absence of the mutation, or the presence or amount of
CC expression of the polypeptide). The human G-protein coupled receptor
CC polypeptide or polynucleotide can be used for diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject,
CC and for preventing, treating or ameliorating a medical condition, such as
CC a disorder related to aberrant G-protein coupled receptor activity, a
CC disorder related to aberrant signal transduction, a reproductive disorder
CC; a male reproductive disorder, a testicular disorder, a vas deferens
CC disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,
CC epididymitis, genital warts, germinal cell aplasia, cryptorchidism,
CC varicocele, immotile cilia syndrome, viral orchitis, sperm transport
CC disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,
CC testicular germ cell tumours, male hormone disorders, premature puberty,
CC incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune
CC disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,
CC immunodeficiency diseases such as AIDS, rheumatoid arthritis,
CC granulomatous disease, inflammatory bowel disease, sepsis, acne,
CC neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell
CC mediated cytotoxicity, immune reactions to transplanted organs and
CC tissues, such as host-versus-graft and graft-versus-host diseases, or
CC autoimmunity disorders, such as autoimmune infertility, demyelination,
CC systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's
CC disease, scleroderma, T-cell maturation disorders, B-cell maturation
CC disorders, vascular disorders, stroke, ischaemia, myocardial infarction,
CC atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,
CC irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,
CC endocrine disorders, or ovarian, stomach, colon or kidney cancer or its
CC related proliferative condition (many other diseases and disorders are
CC listed in the specification). The antibodies may be used to purify,
CC detect and target the G-protein coupled receptor polypeptides. The
CC polynucleotides are also useful in gene therapy. The present sequence
CC encodes a novel GPCR of the invention.

XX
SQ Sequence 2685 BP; 404 A; 906 C; 882 G; 493 T; 0 U; 0 Other;

Query Match 60.6%; Score 2157.4; DB 12; Length 2685;
Best Local Similarity 84.6%; Pred. No. 0;
Matches 2684; Conservative 0; Mismatches 1; Indels 486; Gaps 4;

QY 211 ATGCTGGGCCCTGCTGCTGGGCCCTCAGCCTCTGGGCTCTCTGCACCCCTGGGACGGG 270
Db |||||
QY 271 GCCCCATTGCTGCTGCACAGCACTTAGGATGAAGGGGACTACGTCTGGGGGGCTG 330
Db |||||
QY 61 GCCCCATTGCTGCTGCACAGCACTTAGGATGAAGGGGACTACGTCTGGGGGGCTG 120
QY 331 TTCCCCCTGGGCGAGGCCGAGGAGGTGGCCTCCGACCGGACACGGCCCGAGCCCT 390
Db |||||
QY 121 TTCCCCCTGGGCGAGGCCGAGGAGGTGGCCTCCGACCGGACACGGCCCGAGCCCT 180
QY 391 GTGTGCACCAAGGTACAGAGGTGGGACCGCCTGGGTCTGGGTCTAGGTGACCAAGGTCTGGG 450
Db |||||

Db 181 GTGTGCA----- 187
QY 451 GTGCTCCTGAGCTGGGCGGAGGTGGCCATCTGGGTTCTGTGTGGCCCCAGGTTCTCCT 510
Db 188 -----CCAGGTTCTCCT 199
QY 511 CAAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCCGTGGAGGAGATCAACAACAAAGT 570
Db 200 CAAACGGCCTGCTCTGGGCACTGGCCATGAAATGGCCGTGGAGGAGATCAACAACAAAGT 259
QY 571 CGGATCTGCTGCCCCGGCTGGGCTGGGCTACGACCTCTTTGATACGTCGAGCCTG 630
Db 260 CGGATCTGCTGCCCCGGCTGGGCTGGGCTACGACCTCTTTGATACGTCGAGCCTG 319
QY 631 TGGTGGCCATGAAGCCAGCCTCATGTTCTTGGCCAAAGCAGGCAGCCGCGACATCGCCG 690
Db 320 TGGTGGCCATGAAGCCAGCCTCATGTTCTTGGCCAAAGCAGGCAGCCGCGACATCGCCG 379
QY 691 CCTACTGCAACTACACGCACTACAGCCAGCCCGCTGTGCTGGCTCATCGGGCCCCACTCGT 750
Db 380 CCTACTGCAACTACACGCACTACAGCCAGCCCGCTGTGCTGGCTCATCGGGCCCCACTCGT 439
QY 751 CAGAGCTGCCCAGTGGTCAACGGCAAGTTCTTTCAGCTTCTTCTCATGCCCCAGTGGGGG 810
Db 440 CAGAGCTGCCCAGTGGTCAACGGCAAGTTCTTTCAGCTTCTTCTCATGCCCC----- 489
QY 811 CCCCCACCATACCCACCCCAACCAACCCCTGCCCCGTGGGAGCCCCCTTGTGTACGGA 870
Db 490 ----- 489
QY 871 GAATGCTACATGACACCCCAACCCAGCCCTGCCCTGGGAGCCCTGTGTCAAGAATGCTCTT 930
Db 490 ----- 489
QY 931 GGCCTTTCAGGTTCAGTACGGTGTAGCATGGAGTGTGAGGCGCCCGGAGACCTTCCC 990
Db 490 -----CAGGTTCAGTACGGTGTAGCATGGAGTGTGAGGCGCCCGGAGACCTTCCC 542
QY 991 CTCCTTCTTCCGACCCGTGCCCCAGCGACCGTGTGAGCTGACGGCGCCCGCGGAGCTGCT 1050
Db 543 CTCCTTCTTCCGACCCGTGCCCCAGCGACCGTGTGAGCTGACGGCGCCCGCGGAGCTGCT 602
QY 1051 GCAGGAGTTCCGCTGGAACCTGGGTGGCCCGCTGGGCGACGACGAGTACGGCCCGCA 1110
Db 603 GCAGGAGTTCCGCTGGAACCTGGGTGGCCCGCTGGGCGACGACGAGTACGGCCCGCA 662
QY 1111 GGGCCTGAGCATCTTCTCGGCCCTGGCCCGGCGACGCGGCATCTGATCGCGCACGAGGG 1170
Db 663 GGGCCTGAGCATCTTCTCGGCCCTGGCCCGGCGACGCGGCATCTGATCGCGCACGAGGG 722
QY 1171 CCTGGTGCCGTGCCCCGTGCCGATGACTCGCGGCTGGGAAAGGTGACGACGTCCTGCA 1230
Db 723 CCTGGTGCCGTGCCCCGTGCCGATGACTCGCGGCTGGGAAAGGTGACGACGTCCTGCA 782
QY 1231 CCAGGTGAACCAAGACAGCGCTGCAGGTGGTGTGCTGTTTCGCCCTCCGTGACGCCGCCA 1290
Db 783 CCAGGTGAACCAAGACAGCGCTGCAGGTGGTGTGCTGTTTCGCCCTCCGTGACGCCGCCA 842
QY 1291 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTTCGCCCAAGGTGTGGGTGGCCAGCGA 1350
Db 843 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTTCGCCCAAGGTGTGGGTGGCCAGCGA 902
QY 1351 GGCCTGGCTGACCTCTGACCTGGTTCATGGGGTGGCCGATGGCCCGATGGGACCGGT 1410
Db 903 GGCCTGGCTGACCTCTGACCTGGTTCATGGGGTGGCCGATGGCCCGATGGGACCGGT 962
QY 1411 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACAGATTCCCCCAGTACCTGAAAGACGCA 1470
Db 963 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACAGATTCCCCCAGTACCTGAAAGACGCA 1022
QY 1471 CCTGGCCCTGGCCACCGACCCGGCCTTCTGCTGTCCTGGGCGAGAGGAGCAGGGTCT 1530
Db 1023 CCTGGCCCTGGCCACCGACCCGGCCTTCTGCTCTGCTGCTGGGCGAGAGGAGGAGGAGGCTCT 1082

QY 1531 GGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGACTGCATCACGCTGCAGAACGT 1590
Db 1083 GGAGGAGGACGTGGTGGCCAGCGCTGCCCGAGTGTGACTGCATCACGCTGCAGAACGT 1142
QY 1591 GAGCGCAGGGCTAAATCACCAACAGACGTTTCTTGTCTACGCAGCTGTGTATAGCGTGGC 1650
Db 1143 GAGCGCAGGGCTAAATCACCAACAGACGTTTCTTGTCTACGCAGCTGTGTATAGCGTGGC 1202
QY 1651 CCAGGCCCTGCACAAACACTTTCAGTGCAACGCCCTCAGGCTGCCCGCGCAGGACCCCGT 1710
Db 1203 CCAGGCCCTGCACAAACACTTTCAGTGCAACGCCCTCAGGCTGCCCGCGCAGGACCCCGT 1262
QY 1711 GAAAGCCCTGGCAGGTGAGCCCGGAGATGGGGGTGTGTCTCTCTGCAATGTGCCAGGC 1770
Db 1263 GAAAGCCCTG----- 1271
QY 1771 CACCAGGCACGGCCACCAACGCTGAGCTGGAGGTGGCTGGCGGCTCAGCCCGCTCCCCCG 1830
Db 1272 ----- 1271
QY 1831 CCCCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGCGGGCTGCCGCTGCG 1890
Db 1272 ---GCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGCGGGCTGCCGCTGCG 1328
QY 1891 GTTCGACAGCAGCGGAAACCTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1950
Db 1329 GTTCGACAGCAGCGGAAACCTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1388
QY 1951 CTCAGTCCCCAGGCTCCACGACGTGGGCGAGGTTCAACGGCAGCCTCAGGACAGAGCGCT 2010
Db 1389 CTCAGTCCCCAGGCTCCACGACGTGGGCGAGGTTCAACGGCAGCCTCAGGACAGAGCGCT 1448
QY 2011 GAAGATCCGCTGGCACACGCTCTGACAAACAGGTGAGGTGAGGTGGGTGTGCCAGGCGTG 2070
Db 1449 GAAGATCCGCTGGCACACGCTCTGACAAACAGGT----- 1481
QY 2071 CCGCTGGTAGCCCCCGCGGACAGGCGCAGCCTTGGGGGTGGGGCGGCTTCCAGTCTCCCGT 2130
Db 1482 ----- 1481
QY 2131 GGGCATGCCACGCCGAGCAGAGCCAGACCCAGGCCCTGTGCGCAGAAAGCCCGTGTCCCGG 2190
Db 1482 -----GCCCGTGTCCCGG 1494
QY 2191 TGCTCGCGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCACCTCCTGTGC 2250
Db 1495 TGCTCGCGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCACCTCCTGTGC 1554
QY 2251 TACGACTGTGTGGACTGCGAGGGGGCAGCTACCGGCAAAACCCAGGTGAGCCGCTTCC 2310
Db 1555 TACGACTGTGTGGACTGCGAGGGCGGAGCTACCGGCAAAACCCAGGTGAGCCGCTTCC 1614
QY 2311 CGGAGGGGGGTGGAAACGACAGAGGGGAGGTCCTGCCAAGTCTTACTCTGAGACC 2370
Db 1615 CGGAGGGGGGTGGAAACGACAGAGGGGAGGTCCTGCCAAGTCTTACTCTGAGACC 1674
QY 2371 AGAGCCCCACAGGTTAAGACGAACACCCAGCGCCCTTCTCCTCTCTCACAGACGACATC 2430
Db 1675 AGAGCCCCACAGGTTAAGACGAACACCCAGCGCCCTTCTCCTCTCTCACAGACGACATC 1734
QY 2431 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACAGCTGCTTCCGC 2490
Db 1735 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACAGCTGCTTCCGC 1794
QY 2491 CGCAGGTCTCGGTTCTTGGCATGGGGCGAGCGGCTGTGCTGCTGCTGCTGCTGCTG 2550
Db 1795 CGCAGGTCTCGGTTCTTGGCATGGGGCGAGCGGCTGTGCTGCTGCTGCTGCTGCTG 1854
QY 2551 AGCCTGGCGCTGGGCTTGTGCTGGCTGCTTGGGGCTGTTGGTTCACCATCGGACAGC 2610
Db 1855 AGCCTGGCGCTGGGCTTGTGCTGGCTGCTTGGGGCTGTTGGTTCACCATCGGACAGC 1914

QY 2611 CCACTGGTTACGGCTCGGGGGGGCCCTGGCTGCTTTGGCCTGGTGTGCTGGGCCTG 2670
Db |||||
QY 1915 CCACTGGTTACGGCTCGGGGGGGCCCTGGCTGCTTTGGCCTGGTGTGCTGGGCCTG 1974
Db |||||
QY 2671 GTCTGCCTCAGCGTCCTCCTGTTCCCTGGCCAGCCAGCCCTGCCGATGCTGGCCAG 2730
Db |||||
QY 1975 GTCTGCCTCAGCGTCCTCCTGTTCCCTGGCCAGCCAGCCCTGCCGATGCTGGCCAG 2034
Db |||||
QY 2731 CAGCCCTTGTCCACCTCCCGCTACGGGCTGCTGAGCACACTCTTCTGTCAGGCGGC 2790
Db |||||
QY 2035 CAGCCCTTGTCCACCTCCCGCTACGGGCTGCTGAGCACACTCTTCTGTCAGGCGGC 2094
Db |||||
QY 2791 GAGATCTTCGTGGAGTCAGAACTGCCTTGAGCTGGCAGACCGGCTGAGTGGCTG 2850
Db |||||
QY 2095 GAGATCTTCGTGGAGTCAGAACTGCCTTGAGCTGGCAGACCGGCTGAGTGGCTG 2154
Db |||||
QY 2851 CGGGGGCCCTGGCCCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2910
Db |||||
QY 2155 CGGGGGCCCTGGCCCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2214
Db |||||
QY 2911 ACCTGGTACCTGGTGGCCCTTCCCGCCGGAGGTGGTGACGGACTGGCACATGCTGCCACG 2970
Db |||||
QY 2215 ACCTGGTACCTGGTGGCCCTTCCCGCCGGAGGTGGTGACGGACTGGCACATGCTGCCACG 2274
Db |||||
QY 2971 GAGGCGTGGTGCACTGCCCGCACACGCTCCTGGGTGAGTTTCGGCTAGCGCACGCCACC 3030
Db |||||
QY 2275 GAGGCGTGGTGCACTGCCCGCACACGCTCCTGGGTGAGTTTCGGCTAGCGCACGCCACC 2334
Db |||||
QY 3031 AATGCCACGCTGGCCCTTCTCTGCTTCTGCTGGGCACCTTCTGCTGGGAGCCAGCCGGGC 3090
Db |||||
QY 2335 AATGCCACGCTGGCCCTTCTCTGCTTCTGCTGGGCACCTTCTGCTGGGAGCCAGCCGGGC 2394
Db |||||
QY 3091 TGCTACAAACCGTGGCCCTGGCCCTCACCTTTGCCATGCTGGCTACTTCATCACCTGGGTC 3150
Db |||||
QY 2395 CGCTACAAACCGTGGCCCTGGCCCTCACCTTTGCCATGCTGGCTACTTCATCACCTGGGTC 2454
Db |||||
QY 3151 TCCTTTGTGCCCCCTCCTGGCCAAATGTGCAGGTGGTCTCAGGCCCGCCGTGCAGATGGGC 3210
Db |||||
QY 2455 TCCTTTGTGCCCCCTCCTGGCCAAATGTGCAGGTGGTCTCAGGCCCGCCGTGCAGATGGGC 2514
Db |||||
QY 3211 GCCCTCCTGCTCTGTGCTCCTGGGCATCCTGGCTGCCCTTCCACCTGCCAGGTGTACCTG 3270
Db |||||
QY 2515 GCCCTCCTGCTCTGTGCTCCTGGGCATCCTGGCTGCCCTTCCACCTGCCAGGTGTACCTG 2574
Db |||||
QY 3271 CTCATGCGGCAGCCAGGGCTCAACACCCCGAGTTCTTCTGGGAGGGGCCCTGGGGAT 3330
Db |||||
QY 2575 CTCATGCGGCAGCCAGGGCTCAACACCCCGAGTTCTTCTGGGAGGGGCCCTGGGGAT 2634
Db |||||
QY 3331 GCCCAAGGCCAGAAATACGGGAACACAGGAAATCAGGGGAACATGAGTGA 3381
Db |||||
QY 2635 GCCCAAGGCCAGAAATACGGGAACACAGGAAATCAGGGGAACATGAGTGA 2685
Db |||||

RESULT 10
AAS14574
ID AAS14574 standard; cDNA; 3489 BP.
XX
AC AAS14574;
XX
DT 18-DEC-2001 (first entry)
DE Human cDNA encoding G protein-coupled receptor, GPCR, 50289.
XX
KW Human; ss; GPCR; G protein-coupled receptor; 50289; cardiant;
KW antithrombotic; analgesic; cytosolic; antiangiogenic;
KW cardiovascular disorder; angiogenesis-related disorder; neural disorder;
KW pain response disorder; inflammatory disorder; atherosclerosis;
KW angina pectoris; myocardial infarction; ischaemic heart disease;
KW sudden cardiac death; obesity; hypertensive heart disease; diabetes;
KW prostate cancer-related pain.
OS Homo sapiens.
XX

PH Key Location/Qualifiers
FT CDS 52..2610
FT /*tag= a
FT /product= "GPCR50289"
FT sig_peptide /note= "This region is specifically claimed in claim 2"
FT 52..111
FT /*tag= b
FT mat_peptide 112..2607
FT /*tag= c
FT /label= Mature_GPCR50289
XX
PN WO200164882-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006543.
XX
PR 29-FEB-2000; 2000US-0186059P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Galvin KM, Silos-Santiago I;
XX
XX WPI; 2001-589866/66.
DR P-PSDB; AAU08996.
XX
PT Novel G protein coupled receptors and nucleic acids encoding them, for
identifying agents for the treatment of cardiac disorders.
PS Claim 2; Fig 15; 209pp; English.
XX
CC The invention relates to novel human G protein-coupled receptors (GPCR)
named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and
nucleic acids encoding them are useful for identifying agents for the
treatment of cardiovascular disorders, angiogenesis-related disorders,
neural disorders, pain response disorders and inflammatory disorders e.g.
atherosclerosis, angina pectoris and myocardial infarction, ischaemic
heart disease, sudden cardiac death, hypertensive heart disease,
diabetes, prostate cancer-related pain, diabetes and obesity. The present
sequence encodes GPCR 50289
SQ Sequence 3489 BP; 578 A; 1189 C; 1102 G; 612 T; 0 U; 8 Other;

Query Match 58.9%; Score 2099.2; DB 4; Length 3489;
Best Local Similarity 81.6%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 13; Indels 612; Gaps 5;
QY 170 GGGGAGCCACCTGCCCTGCTGTTGGAAGTTGCCCTGCTGCCATGCTGGGCCCTGCTGTC 229
Db |||||
QY 230 TGGGCTCAGCCCTCTGGGCTCTCCTGCACCCCTGGGAGCGGGGCCCATTTGTCCTGTCAC 289
Db |||||
QY 71 TGGGCTCAGCCCTCTGGGCTCTCCTGCACCCCTGGGAGCGGGGCCCATTTGTCCTGTCAC 130
QY 290 AGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGGCTGTTCCCTGGGAGGCGCG 349
Db |||||
QY 131 AGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGGCTGTTCCCTGGGAGGCGCG 190
QY 350 AGGAGGCTGGCTCCCGCAGCCGACACGGCCAGCAGCCCTGTGTGCACAGGTACAGAG 409
Db |||||
QY 191 AGGAGGCTGGCTCCCGCAGCCGACACGGCCAGCAGCCCTGTGTGCA----- 238
QY 410 GTGGGACGGCTGGGTCGGGTCAGGTCAGGTCAGGTCAGGTCAGTGGGTCCTGAGCTGGGCC 469
Db |||||
QY 239 ----- 238
QY 470 GAGGTGGCCATCTGCGGTTCTGTGTGGCCCGCAGGTTCTCTCAAACGGCTGCTGCGGC 529
Db |||||
QY 239 -----CCAGGTTCTCTCAAACGGCTGCTGCGGC 269
QY 530 ACTGGCCATGAATAATGGCCGTGGAGGAGATCAACAAGTCGGATCTGTCGCCGGCT 589
Db |||||

Db	270	ACTGGCCATGAAATGGCCGTGGAGAGATCAACAACAGTCGGATCTGCTGCCGGGCT	329
QY	590	CGCCCTGGGCTACGACCTCTTTGATACGTGCTCGAGCCCTGTGGTGGCCATGAAGCCACG	649
Db	330	CGCCCTGGGCTACGACCTCTTTGATACGTGCTCGAGCCCTGTGGTGGCCATGAAGCCACG	389
QY	650	CCTCATGTTCTTGGCCAAAGCAGGACGCGCGACATCGCCGCTACTGCAACTACACGCA	709
Db	390	CCTCATGTTCTTGGCCAAAGCAGGACGCGCGACATCGCCGCTACTGCAACTACACGCA	449
QY	710	GTACCAGCCCCGTGTGCTGGCTGTCTCTCATGCCCCAGTGGGGCGCCCCACCATCACCCACC	769
Db	450	GTACCAGCCCCGTGTGCTGGCTGTCTCTCATGCCCCAGTGGGGCGCCCCACCATCACCCACC	509
QY	770	CGCAAGTTCTTACAGCTTCTTCCATGCCCCAGTGGGGCGCCCCACCATCACCCACC	829
Db	510	CGCAAGTTCTTACAGCTTCTTCCATGCCCCAGTGGGGCGCCCCACCATCACCCACC	540
QY	830	CCCAACCAACCCCTGCCCGTGGAGCCCTTGTGTACGAGAAATGTACATGCACCCCA	889
Db	541	-----	540
QY	890	CCCAGCCCTGCCCTGGAGCCCTGTGTACGAAATGCTCTTGGCCCTGCAGGTACAGCTAC	949
Db	541	-----	552
QY	950	GGTGCTAGCATGGAGCTGTGAGCGCCCGGGAGACCTTCCCCCTCTTCTTCCGACCGTG	1009
Db	553	GGTGCTAGCATGGAGCTGTGAGCGCCCGGGAGACCTTCCCCCTCTTCTTCCGACCGTG	612
QY	1010	CCCAGCACCGTGTGAGCTGACGGCCCGCGGAGCTGCTGCAGGAGTTTGGCTGGAAC	1069
Db	613	CCCAGCACCGTGTGAGCTGACGGCCCGCGGAGCTGCTGCAGGAGTTTGGCTGGAAC	672
QY	1070	TGGGTGGCCGCCCTGGGACGACGACGAGTACGGCCGGCAGGGCCTGAGCATCTTCTCG	1129
Db	673	TGGGTGGCCGCCCTGGGACGACGACGAGTACGGCCGGCAGGGCCTGAGCATCTTCTCG	732
QY	1130	GCCCTGGCCCGGCACGGCGCATCTGCATCGCGCACGAGGGCCTGGTGCCGCTGCCCGCT	1189
Db	733	GCCCTGGCCCGGCACGGCGCATCTGCATCGCGCACGAGGGCCTGGTGCCGCTGCCCGCT	792
QY	1190	GCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTGCACCAGGTGAACAGAGCAGC	1249
Db	793	GCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTGCACCAGGTGAACAGAGCAGC	852
QY	1250	GTGAGGTGGTGTGCTGTTCGCCCTCCGTGCACGCGCGCCACGCCCTCTTCAACTACAGC	1309
Db	853	GTGAGGTGGTGTGCTGTTCGCCCTCCGTGCACGCGCGCCACGCCCTCTTCAACTACAGC	912
QY	1310	ATCAGCAGCAGGCTCTGCCCAAGGTGTGGTGGCGCAGCGCCCTGGCTGACCTCTGAC	1369
Db	913	ATCAGCAGCAGGCTCTGCCCAAGGTGTGGTGGCGCAGCGCCCTGGCTGACCTCTGAC	972
QY	1370	CTGCTCATGGGGTGCCTGCCGATGGCCAGATGGGCACGGTGTGGCTTCTTCCAGAGG	1429
Db	973	CTGCTCATGGGGTGCCTGCCGATGGCCAGATGGGCACGGTGTGGCTTCTTCCAGAGG	1032
QY	1430	GGTGCCAGCTGCACGAGTTCCCCAGTACGTGAAGACGACACCTGGCCCTGGCCACCGAC	1489
Db	1033	GGTGCCAGCTGCACGAGTTCCCCAGTACGTGAAGACGACACCTGGCCCTGGCCACCGAC	1092
QY	1490	CCGGCTTCTGCTCTGCCCTGGGCGAGGGAGCAGGGTCTGAGGAGGACGCTGCTGGGC	1549
Db	1093	CCGGCTTCTGCTCTGCCCTGGGCGAGGGAGCAGGGTCTGAGGAGGACGCTGCTGGGC	1152
QY	1550	CAGCGTGGCCGAGTGTGATGCACTACGCTGCAGAACGTGAGCGCAGGGCTAAATCAC	1609
Db	1153	CAGCGTGGCCGAGTGTGATGCACTACGCTGCAGAACGTGAGCGCAGGGCTAAATCAC	1212
QY	1610	CACCAGACGTTCTGTCTACGCGTGTGTATAGCGTGGCCAGGCCCTGCACACACT	1669
Db	1213	CACCAGACGTTCTGTCTACGCGTGTGTATAGCGTGGCCAGGCCCTGCACACACT	1272

QY	1670	CTTCAGTGAACGCGCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGC	1729
Db	1273	CTTCAGTGAACGCGCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTG	1322
QY	1730	CCGGGAGATGGGGGTGTGCTGTCTCTGTCAATGTGCCACAGGCCACAGGCACGGCCACCAC	1789
Db	1323	-----	1322
QY	1790	GCCTGAGCTGGAGGTGGCTGGCGGCTCAGCCCCCGTCCCCCGCCGACGCTCCTGGAGAAC	1849
Db	1323	-----GCAGCTCCTGGAGAAC	1338
QY	1850	ATGTACAACCTGACCTTCCACGTGGCGGGCTGCCGCTGCGGTTTCGACAGCAGCGGAAC	1909
Db	1339	ATGTACAACCTGACCTTCCACGTGGCGGGCTGCCGCTGCGGTTTCGACAGCAGCGGAAC	1398
QY	1910	GTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCAGGCTCCAC	1969
Db	1399	GTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCAGGCTCCAC	1458
QY	1970	GACGTGGGCAGGTTCAACGGCAGCCTCAGGACAGAGCGCTGAAGATCCGCTGGCACACG	2029
Db	1459	GACGTGGGCAGGTTCAACGGCAGCCTCAGGACAGAGCGCTGAAGATCCGCTGGCACACG	1518
QY	2030	TCTGACAACGAGGTGAGGTGAGGGTGGGTGTGCCAGGCGTGCCCGGTAGCCCCCGCGG	2089
Db	1519	TCTGACAAC	1527
QY	2090	CAGGGCGCAGCCTGGGGGTGGGGCGGTTCCAGTCTCCCGTGGGCATGCCAGCCGAGCA	2149
Db	1528	-----	1527
QY	2150	GAGCCAGACCCAGGCTGTGCGCAGAAAGCCGCTGTCCCGTGTCCCGCAGTGCCAGG	2209
Db	1528	-----CAGAAGCCCGTGTCCCGATGCTCGCGCAGTGCCAGG	1564
QY	2210	AGGGCCAGGTGCGCCGGGTCAAGGGTTCCACTCTGCTGCTACGACTGTGTGGACTGCG	2269
Db	1565	AGGGCCAGGTGCGCCGGGTCAAGGGTTCCACTCTGCTGCTACGACTGTGTGGACTGCG	1624
QY	2270	AGCGGGCAGCTACCGGCAAAACCCAGGTGAGCCGCTTCCCGGCAGGCGGGGTGGAA	2329
Db	1625	AGCGGGCAGCTACCGGCAAAAC	1648
QY	2330	CGCAGCAGGGAGGGTCTGTGCCAAGTCTCTGACTCTGAGACCAGAGCCACAGGGTACAAG	2389
Db	1649	-----	1648
QY	2390	ACGAACACCCAGCGCCCTCTCTCTCTCACAGACGACATCGCCTGCACCTTTGTGGCC	2449
Db	1649	-----CAGACGACATCGCCTGCACCTTTGTGGCC	1678
QY	2450	AGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCGCAGGTCTCGGTTCTCTGG	2509
Db	1679	AGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCGCAGGTCTCGGTTCTCTGG	1738
QY	2510	CATGGGCGAGCCGGCTGTGCTGCTGCTGCTCCTCTGCTGCTGAGCCCTGGCGCTGGGCTTG	2569
Db	1739	CATGGGCGAGCCGGCTGTGCTGCTGCTCCTCTGCTGCTGAGCCTGGCGCTGGGCTTG	1798
QY	2570	TGCTGGCTGCTTTGGGGCTGTTCGTTACCAATCGGGACAGCCCACTGGTTACGGCTCGG	2629
Db	1799	TGCTGGCTGCTTTGGGGCTGTTCGTTACCAATCGGGACAGCCCACTGGTTACGGCTCGG	1858
QY	2630	GGGGGCCCCCTGGCCTGCTTTGGGCTGGTGTGCTGGGCTGGTCTGCTCAGGCTCCTCC	2689
Db	1859	GGGGGCCCCCTGGCCTGCTTTGGGCTGGTGTGCTGGGCTGGTCTGCTCAGGCTCCTCC	1918
QY	2690	TGTTCCCTGGCCAGCCCGCTGCTGCTGCTGGCCAGCAGCCCTTGTCCCACTCC	2749
Db	1919	TGTTCCCTGGCCAGCCCGCTGCTGCTGCTGGCCAGCAGCCCTTGTCCCACTCC	1978

QY 2750 CGCTACGGGCTGCCTGAGCACACTCTTCTGTCAGGGCGCGAGATCTTCGTGGAGTCAG 2809
Db |||||
1979 CGCTACGGGCTGCCTGAGCACACTCTTCTGTCAGGGCGCGAGATCTTCGTGGAGTCAG 2038
QY 2810 AACTGCCCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGGCCTGGC 2869
Db |||||
2039 AACTGCCCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGGCCTGGC 2098
QY 2870 TGGTGGTGTCTGCTGGCCATGCTGGTGGAGGTGCACTGTGCACCTGGTACCTGGTGGCCT 2929
Db |||||
2099 TGGTGGTGTCTGCTGGCCATGCTGGTGGAGGTGCACTGTGCACCTGGTACCTGGTGGCCT 2158
QY 2930 TCCCGCGGAGGTGGTGACGGACTGGCAATGTCACCATGTCGCCACGAGGCGCTGGTGCACCTGCC 2989
Db |||||
2159 TCCCGCGGAGGTGGTGACGGACTGGCAATGTCGCCACGAGGCGCTGGTGCACCTGCC 2218
QY 2990 GCACACGCTCCTGGGTGAGTTCGGCTAGCGCACGCCACCAATGCCACGCTGGCCTTTC 3049
Db |||||
2219 GCACACGCTCCTGGGTGAGTTCGGCTAGCGCACGCCACCAATGCCACGCTGGCCTTTC 2278
QY 3050 TCTGCTTCTTGGGCACCTTCTGCTGGTGGGAGCGCAGCGGGCTGTACAAACCGTGCCTGGT 3109
Db |||||
2279 TCTGCTTCTTGGGCACCTTCTGCTGGTGGGAGCGCAGCGGGCTGTACAAACCGTGCCTGGT 2338
QY 3110 GCCTACCTTTGCCATGCTGGCTTACTTCACTGCTGGGTCTCTTTGTGCCCTCCTGG 3169
Db |||||
2339 GCCTACCTTTGCCATGCTGGCTTACTTCACTGCTGGGTCTCTTTGTGCCCTCCTGG 2398
QY 3170 CCAATGTGCAGGTGGTCTCAGGCCGCGCGTGCAGATGGGCGCCTCCTGCTCTGTGTCC 3229
Db |||||
2399 CCAATGTGCAGGTGGTCTCAGGCCGCGCGTGCAGATGGGCGCCTCCTGCTCTGTGTCC 2458
QY 3230 TGGGCATCCTGGTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGCGGCAGCCAGGCG 3289
Db |||||
2459 TGGGCATCCTGGTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGCGGCAGCCAGGCG 2518
QY 3290 TCAACACCCCGAGTTCTTCTGGGAGGGGCGCCTGGGGATGCCCAAGGCCAGAATGACG 3349
Db |||||
2519 TCAACACCCCGAGTTCTTCTGGGAGGGGCGCCTGGGGATGCCCAAGGCCAGAATGACG 2578
QY 3350 GGAACACAGGAAATCAGGGGAAACATGAGTGACCCAAACCTGTGATCTCAGCCCCGGTGA 3409
Db |||||
2579 GGAACACAGGAAATCAGGGGAAACATGAGTGACCCAAACCTGTGATCTCAGCCCCGGTGA 2638
QY 3410 ACCCAGACTTAGCTGCGATCCCCCCCCAAGCCAGCAATGACCGTGTCTCGCTACAGAGAC 3469
Db |||||
2639 ACCCAGACTTAGCTGCGATCCCCCCCCAAGCCAGCAATGACCGTGTCTCGCTACAGAGAC 2698
QY 3470 CCTCCCGCTCTAGGTTCTGACCCCGAGTTGTCTCCTGACCTGACCCACAGTGAGCCCT 3529
Db |||||
2699 CCTCCCGCTCTAGGTTCTGACCCCGAGTTGTCTCCTGACCTGACCCACAGTGAGCCCT 2758
QY 3530 AGGCCTGGAGCACGTGGACACCCCTGTGACCATC 3563
Db |||||
2759 AGGCCTGGAGCACGTGGACACCCCTGTGACCATC 2792

RESULT 11
ADG19751

ID ADG19751 standard; cDNA; 3489 BP.

AC ADG19751;

XX 26-FEB-2004 (first entry)

DT Human G protein coupled receptor (GPCR) 50289 cDNA.

XX cytosolic; nephrotropic; antiinflammatory; cardiant; respiratory;
KW gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
KW 18636; 2466; 43238; 1983; 52881; 2398; 45449; 50289; 52872; 26908;
KW cellular proliferative disorder; brain disorder; renal disorder;
KW kidney disorder; inflammatory disorder; cardiovascular disorder;
KW liver disorder; intestinal disorder; respiratory disorder;

KW angiogenic disorder; human; G protein coupled receptor; GPCR; gene; ss.
XX Homo sapiens.
OS
XX US2003215860-A1.
XX 20-NOV-2003.
XX 03-APR-2003; 2003US-00407079.
PF 29-FEB-2000; 2000US-0186059P.
XX 24-MAR-2000; 2000US-0191845P.
PR 22-MAY-2000; 2000US-0206019P.
PR 17-NOV-2000; 2000US-00715790.
PR 28-FEB-2001; 2001US-00796338.
PR 22-MAY-2001; 2001US-00863200.
PR 22-AUG-2001; 2001US-0314041P.
PR 22-AUG-2001; 2001US-0314185P.
PR 21-AUG-2002; 2002US-00225094.
PR 22-AUG-2002; 2002US-00226102.
PR 15-OCT-2002; 2002US-00272417.
PR 29-OCT-2002; 2002US-00282837.
XX (MILL-) MILLENNIUM PHARM INC.
PA Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;
XX WPI; 2004-010777/01.
PI P-PSDB; ADG19752.
XX New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
DR 45449, 50289, 52872 or 26908, useful in preparing a composition for
DR treating e.g., cellular proliferative, brain, kidney, inflammatory or
XX angiogenic disorder.
PS Claim 2; SEQ ID NO 89; 163pp; English.
XX The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
CC 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
CC sequence comprising 939-3489 bp or its fragment comprising at least 15
CC nucleotides; a sequence encoding a polypeptide comprising a sequence
CC having 223-852 amino acids, or its allelic variant or fragment comprising
CC at least 15 contiguous amino acids; or a sequence that hybridises with
CC (1) under stringent conditions. The nucleic acid or polypeptide is useful
CC in preparing a composition for treating a disorder characterised by
CC aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
CC 26908 activity e.g., cellular proliferative, brain, renal, kidney,
CC inflammatory, cardiovascular, liver, intestinal, respiratory or
CC angiogenic disorder. This sequence encodes novel human protein 50289, a G
CC protein coupled receptor (GPCR).
XX Sequence 3489 BP; 578 A; 1189 C; 1102 G; 612 T; 0 U; 8 Other;
SQ Query Match 58.9%; Score 2099.2; DB 12; Length 3489;
Best Local Similarity 81.6%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 13; Indels 612; Gaps 5;
QY 170 GGGGCAGCCACCTGCCCTGCTGTTGGAAGTTGCTGTGCCATGCTGGGCCCTGTGTCC 229
Db |||||
11 GAGTCGACCCACTGCGTCCGCTGTTGGAAGTTGCTGTGCCATGCTGGGCCCTGTGTCC 70
QY 230 TGGGCCTCAGCCTCTGGGCTCTCTGCAACCCTGGGACGGGGCCCATTTGTGCTGTAC 289
Db |||||
71 TGGGCCTCAGCCTCTGGGCTCTCTGCAACCCTGGGACGGGGCCCATTTGTGCTGTAC 130
QY 290 AGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGCTGTTCCCCCTGGGCGAGGCCG 349
Db |||||
131 AGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGCTGTTCCCCCTGGGCGAGGCCG 190
QY 350 AGGAGGCTGGCCTCCGACGCGGACACGGGCCAGCCCTGTGTGACACAGGTACAGAG 409
Db |||||
191 AGGAGGCTGGCCTCCGACGCGGACACGGGCCAGCCCTGTGTGCA----- 238

QY	410	GTGGACGCGCCTGGGTGCGGTTCAGGGTCAAGGTACCAGGTCTGGGTGCTCTGGGTGCTCTGAGCTGGGGCC	469
Dd	239	-----	238
QY	470	GAGGTGGCCATCTCGGTTCTGTGTGSGCCCCCAGGTTCTCTCAAACGGCCTGCTCTGGGC	529
Dd	239	-----CCAGGTTCTCTCAAACGGCCTGCTCTGGGC	269
QY	530	ACTGGCCATGAATAATGGCCGTGGAGGAGATCAACAAGTCGGATCTGCTGCCCGGGCT	589
Dd	270	ACTGGCCATGAATAATGGCCGTGGAGGAGATCAACAAGTCGGATCTGCTGCCCGGGCT	329
QY	590	GCGCCTGGGTACGACCTCTTTTGATACGTGCTCGAGCCTGTGTGGTGGCCATGAAGCCCAG	649
Dd	330	GCGCCTGGGTACGACCTCTTTTGATACGTGCTCGAGCCTGTGTGGTGGCCATGAAGCCCAG	389
QY	650	CCTCATGTTCTTGGCCAAGGCAGGCAGCCGCGACATCGCCGCTACTGTGCAACTACACGCA	709
Dd	390	CCTCATGTTCTTGGCCAAGGCAGGCAGCCGCGACATCGCCGCTACTGTGCAACTACACGCA	449
QY	710	GTACCAGCCCGTGTGCTGGCTGTATCGGSCCCCACTCGTCAGAGTGCCTATGGTCAC	769
Dd	450	GTACCAGCCCGTGTGCTGGCTGTATCGGSCCCCACTCGTCAGAGTGCCTATGGTCAC	509
QY	770	CGGCAAGTTCTTCAGCTTCTTCTCATGCCCAAGTGGGGCGCCCCCACCATCACCCACC	829
Dd	510	CGGCAAGTTCTTCAGCTTCTTCTCATGCCCAAGTGGGGCGCCCCCACCATCACCCACC	540
QY	830	CCCAACCAACCCCTGCCCCGTGGGAGCCCCCTGTGTCAAGAGAATGTACATGCACCCCA	889
Dd	541	-----	540
QY	890	CCCAGCCCTGCCCTGGGAGCCCTGTGTCAAGAGATGCTCTTGGCCCTTGCAGGTCACTAC	949
Dd	541	-----CAGGTCACTAC	552
QY	950	GGTGCTAGCATGGAGCTGTGAGCGCCCGGAGACCTTCCCCTCCTTCTTCGCAACCGTG	1009
Dd	553	GGTGCTAGCATGGAGCTGTGAGCGCCCGGAGACCTTCCCCTCCTTCTTCGCAACCGTG	612
QY	1010	CCCAGCGACCGTGTGCACTGACGGCCCGCGAGCTGTGCAAGAGTTCGGTGGAAAC	1069
Dd	613	CCCAGCGACCGTGTGCACTGACGGCCCGCGAGCTGTGCAAGAGTTCGGTGGAAAC	672
QY	1070	TGGGTGGCCCGCCTGGGACGACGACGAGTACGSCCGGACGGCCCTGAGCATCTTCTCG	1129
Dd	673	TGGGTGGCCCGCCTGGGACGACGACGAGTACGSCCGGACGGCCCTGAGCATCTTCTCG	732
QY	1130	GCCCTGGCCCGGCAACGCGGCATCTGCATCGCGCACGAGGGCCTGGTGCCCTGCCCGCT	1189
Dd	733	GCCCTGGCCCGGCAACGCGGCATCTGCATCGCGCACGAGGGCCTGGTGCCCTGCCCGCT	792
QY	1190	GCCGATGACTCGCGGTGGGAAGGTGCAGGACGTCTGCACCGAGTGAAACAGAGCAGC	1249
Dd	793	GCCGATGACTCGCGGTGGGAAGGTGCAGGACGTCTGCACCGAGTGAAACAGAGCAGC	852
QY	1250	GTGCAGGTGGTGTGCTGTTCGCTCCGTGCACGCGGCCACGCCCCCTTCAAATACAGC	1309
Dd	853	GTGCAGGTGGTGTGCTGTTCGCTCCGTGCACGCGGCCACGCCCCCTTCAAATACAGC	912
QY	1310	ATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCTGGTGAACCTCTGAC	1369
Dd	913	ATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCTGGTGAACCTCTGAC	972
QY	1370	CTGGTCAATGGGCTGCCCGGCATGGCCAGATGGGCACGGTGTGGCTTCTTCCAGAGG	1429
Dd	973	CTGGTCAATGGGCTGCCCGGCATGGCCAGATGGGCACGGTGTGGCTTCTTCCAGAGG	1032
QY	1430	GGTGCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACGACACCTGGCCCTGGCCACCGAC	1489
Dd	1033	GGTGCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACGACACCTGGCCCTGGCCACCGAC	1092
QY	1490	CCGGCCTTCTGCTCTGCCCTGGGCGAGAGGAGCAGGGTCTGGAGGAGGACGTGGTGGGC	1549

Db	1093	 CCGGCCCTTCTGCTCTGCCCTGGCGAGAGGGAGCAGGGTCTGGAGAGGACGTGGTGGGC	1152
QY	1550	CAGCGCTGCCCCGAGTGTGACTGTCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCAC	1609
Db	1153	 CAGCGCTGCCCCGAGTGTGACTGTCATCACGCTGCAGAACGTGAGCGCAGGGCTAAATCAC	1212
QY	1610	CACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTGGCCCCCAGGCCCTGCACAAACACT	1669
Db	1213	 CACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTGGCCCCCAGGCCCTGCACAAACACT	1272
QY	1670	CTTCAGTGCAAACGCTCAGGCTGCCCCCGGCAGGACCCCCGTGAAGCCCTGGCAGGTGAGC	1729
Db	1273	 CTTCAGTGCAAACGCTCAGGCTGCCCCCGGCAGGACCCCCGTGAAGCCCTG-----	1322
QY	1730	CCGGGAGATGGGGTGTGCTGTCTCTGCATGTGCCCCAGGCCACCAGGCACGGCCACCAC	1789
Db	1323	-----	1322
QY	1790	GCCTGAGCTGGAGGTGGCTGGCGGCTCAGCCCCCGTCCCCCGCCCGCAGCTCCTGGAGAAC	1849
Db	1323	-----GCAGCTCCTGGAGAAC	1338
QY	1850	ATGTACAACTGACCTTCCACGTGGCGGGCTGCCGTGCGGTTCGACAGCAGCGGAAAC	1909
Db	1339	 ATGTACAACTGACCTTCCACGTGGCGGGCTGCCGTGCGGTTCGACAGCAGCGGAAAC	1398
QY	1910	GTGGACATGAGTACACACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCTCAGGCTCCAC	1969
Db	1399	 GTGGACATGAGTACACACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCTCAGGCTCCAC	1458
QY	1970	GACGTGGGCAGGTTCAACGGCAGCCTCAGACAGAGCGCCTGAAGATCCGCTGGCACACG	2029
Db	1459	 GACGTGGGCAGGTTCAACGGCAGCCTCAGACAGAGCGCCTGAAGATCCGCTGGCACACG	1518
QY	2030	TCTGACAAACCAGGTGAGGTGAGGGTGGGTGTGCCAGGCGTGCCCCGTGTFAGCCCCCGCGG	2089
Db	1519	 TCTGACAAAC-----	1527
QY	2090	CAGGGCGCAGCCTGGGGGTGGGGCCGTTCCAAGTCTCCCGTGGGCATGCCCCAGCCGAGCA	2149
Db	1528	-----	1527
QY	2150	GAGCCAGACCCCAAGCCTGTGCGCAGAACCCCGTGTCCCGTGTCTCGCGGCAGTGCCAGG	2209
Db	1528	 -----CAGAAAGCCCGTGTCCCGATGTCTCGCGGCAGTGCCAGG	1564
QY	2210	AGGGCCAGGTGCGCCGGGTCAAGGGTTTCCACTCCTGCTGCTACGACTGTGTGGACTGCG	2269
Db	1565	 AGGGCCAGGTGCGCCGGGTCAAGGGTTTCCACTCCTGCTGCTACGACTGTGTGGACTGCG	1624
QY	2270	AGGGGGGCAGCTACCGGCAAAACCCAGGTGAGCCGCTTCCCGCAGCGGGGTGGGAA	2329
Db	1625	 AGGGGGGCAGCTACCGGCAAAACCC-----	1648
QY	2330	CGCAGCAGGGGAGGGTCTCTGCCAAGTCTCTGACTCTGAGACCAAGGCCCCACAGGTFACAAG	2389
Db	1649	-----	1648
QY	2390	ACGAACACCCAGGCCCTTCTCCTCTCTCACAGACGACATCGCCTGCACCTTTTGTGGCC	2449
Db	1649	 -----CAGACGACATCGCCTGCACCTTTTGTGGCC	1678
QY	2450	AGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCCGCAGGTCTCGGTTCCTGG	2509
Db	1679	 AGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCCGCAGGTCTCGGTTCCTGG	1738
QY	2510	CATGGGCGAGCCGGCTGTGCTGCTGCTGCTCTCTGCTGCTGAGCCCTGGCGCTGGGCTTG	2569
Db	1739	 CATGGGCGAGCCGGCTGTGCTGCTGCTGCTCTCTGCTGCTGAGCCCTGGCGCTGGGCTTG	1798
QY	2570	TGCTGGCTGCTTTGGGGCTGTTCTGTTTACCATCGGGACAGCCCCACTGGTTCAGGCCCTCG	2629

Db	1799	TG	TGGCTGCTTTGGGGCTGTTCTCGTTACCATCGGGACAGCCCACTGGTTCAGGCTCGG	1855
QY	2630	GG	GGGCCCCCTGGCCCTGCTTTGGCCCTGGTGTGCCTGGSCCTGGTCTGCCCTCAGCGTCTCTCC	2689
Db	1859	GG	GGGGCCCCCTGGCCCTGCTTTGGCCCTGGTGTGCCTGGSCCTGGTCTGCCCTCAGCGTCTCTCC	1918
QY	2690	TG	TTCCCTGGCCAGCCCCAGCCCTGCCCGATGCCCTGGCCCGCAGCAGCCCTTGTCCACCTCC	2749
Db	1919	TG	TTCCCTGGCCAGCCCCAGCCCTGCCCGATGCCCTGGCCCGCAGCAGCCCTTGTCCACCTCC	1978
QY	2750	CG	CTACGGGCTGCCTGAGCACACTCTTCTCTGACGGCGCCGAGATCTTCGTGAGTCTAG	2809
Db	1979	CG	CTACGGGCTGCCTGAGCACACTCTTCTCTGACGGCGCCGAGATCTTCGTGAGTCTAG	2038
QY	2810	AA	CTGCCTCTGAGCTGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGSCCTGGC	2869
Db	2039	AA	CTGCCTCTGAGCTGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGSCCTGGC	2098
QY	2870	TG	TGGTGGTGTCTGTGGCCATGCTGGTGGAGTGCCTGTGCACCTGTACCTGTGGCCT	2929
Db	2099	TG	TGGTGGTGTCTGTGGCCATGCTGGTGGAGTGCCTGTGCACCTGTACCTGTGGCCT	2158
QY	2930	TC	CCGCCGAGGTGTGACGGACTGGCACATGCTGCCACGGAGCGCTGGTGCACCTGCC	2989
Db	2159	TC	CCGCCGAGGTGTGACGGACTGGCACATGCTGCCACGGAGCGCTGGTGCACCTGCC	2218
QY	2990	GC	ACACGCTCCTGGTCACTTGGCCCTAGCGACGCCACCAATGCCACGCTGGCCTTTC	3049
Db	2219	GC	ACACGCTCCTGGTCACTTGGCCCTAGCGACGCCACCAATGCCACGCTGGCCTTTC	2278
QY	3050	TC	TGCTTCTGGGCACTTCTCTGGTGGGAGCAGCCGGGCTGCTACAAACGCTGCCCGTG	3109
Db	2279	TC	TGCTTCTGGGCACTTCTCTGGTGGGAGCAGCCGGGCTGCTACAAACGCTGCCCGTG	2338
QY	3110	GC	CTACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTCTCCTTTGSCCCTCCTCG	3169
Db	2339	GC	CTACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTCTCCTTTGSCCCTCCTCG	2398
QY	3170	CC	AATGTGAGGTGGTCTCTCAGGCCCGCGCTGCAGATGGCGCCCTCCTGCTCTGTGTCC	3229
Db	2399	CC	AATGTGAGGTGGTCTCTCAGGCCCGCGCTGCAGATGGCGCCCTCCTGCTCTGTGTCC	2458
QY	3230	TG	GGCATCCTGGCTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGGCGCAGCCAGGC	3289
Db	2459	TG	GGCATCCTGGCTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGGCGCAGCCAGGC	2518
QY	3290	TC	AACACCCCCAGTTCCTCTGGGAGGGGCCCTGGGGATGCCAAGGCCAGAATGACG	3349
Db	2519	TC	AACACCCCCAGTTCCTCTGGGAGGGGCCCTGGGGATGCCAAGGCCAGAATGACG	2578
QY	3350	GG	AACACAGGAAATCAGGGAAACATGAGTGACCCACCTGTGATCTCAGCCCCGGTGA	3409
Db	2579	GG	AACACAGGAAATCAGGGAAACATGAGTGACCCACCTGTGATCTCAGCCCCGGTGA	2638
QY	3410	AC	CCAGACTTAGCTGCGATCCCCCAAGCCAGCAATGACCCGTCTCGCTACAGAGAC	3469
Db	2639	AC	CCAGACTTAGCTGCGATCCCCCAAGCCAGCAATGACCCGTCTCGCTACAGAGAC	2698
QY	3470	CT	CCCGCTCTAGGTTCTGACCCCGAGTTGTCTCCTGACCCCTGACCCCAAGTGAGCCCT	3529
Db	2699	CT	CCCGCTCTAGGTTCTGACCCCGAGTTGTCTCCTGACCCCTGACCCCAAGTGAGCCCT	2758
QY	3530	AG	GCCTGGAGCACGTGGACACCCCTGTGACCAATC	3563
Db	2759	AG	GCCTGGAGCACGTGGACACCCCTGTGACCAATC	2792

RESULT 12

ADJ93108

ID ADJ93108 standard; DNA: 3446 BP.

XX

AC XX

DT	06-MAY-2004	(first entry)
XX		
DE	Human G-coupled receptor protein HGPRBMY30 coding sequence.	
XX		
KW	ds; gene; immunosuppressive; cardiant; antiinflammatory; cytostatic;	
KW	anti-HIV; antirheumatic; antiarthritic; antibacterial; antiseborrheic;	
KW	dermatological; antipsoriatic; neuroprotective; nootropic;	
KW	antiparkinsonian; antidiabetic; ophthalmological; antiasthmatic;	
KW	antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive;	
KW	anorectic; metabolic; virucide; osteopathic; antiangular; vulnerary;	
KW	gene therapy; G-protein coupled receptor protein; HGPRBMY30;	
KW	immune disorder; cardiovascular disorder; inflammatory disorder;	
KW	metabolic disorder; reproductive disorder; testicular cancer;	
KW	neural disorder; endocrine disorder; gastrointestinal disorder;	
KW	Alzheimer's disease; Parkinson's diseases; diabetes; dwarfism; asthma;	
KW	schizophrenia; obesity; anorexia; osteoporosis; angina pectoris;	
KW	myocardial infarction.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..2565
FT		/*tag= a
FT		/product= "G-coupled receptor protein HGPRBMY30"
XX		
PN	WO200296946-A1.	
XX		
PD	05-DEC-2002.	
XX		
PF	30-MAY-2002; 2002WO-US017085.	
XX		
PR	30-MAY-2001; 2001US-0294411P.	
XX		
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.	
XX		
PI	Feder JN, Mintier GA, Ramanathan C;	
XX		
DR	WPI; 2003-140445/13.	
DR	P-PSDB; ADJ93109.	
XX		
PT	Novel human G-protein coupled receptor, HGPRBMY30 polypeptide useful for	
PT	preventing and treating e.g. immune disorders, cardiovascular disorders	
PT	or inflammatory disorders.	
XX		
PS	Claim 1; SEQ ID NO 1; 343pp; English.	
XX		
CC	The invention relates to an isolated human G-protein coupled receptor,	
CC	HGPRBMY30 polypeptide or a sequence having 95% identity to the above	
CC	mentioned sequences. (I) is useful for preventing or treating a medical	
CC	condition, selected from an immune disorder; a cardiovascular disorder;	
CC	an inflammatory disorder in which G-protein coupled receptors are either	
CC	directly, or indirectly, associated with the disorder; a metabolic	
CC	disorder; a reproductive disorder; a male reproductive disorder;	
CC	testicular cancer; a neural disorder; an endocrine disorder;	
CC	gastrointestinal disorder; (I) and (II) are also useful for detecting,	
CC	prognosing, preventing, treating, and/or ameliorating the diseases such	
CC	as hematopoietic and pulmonary disorders, Alzheimer's, Parkinson's	
CC	diseases, diabetes, dwarfism, color blindness, retinal pigmentosa,	
CC	asthma, expression, schizophrenia, sleeplessness, hypertension, anxiety,	
CC	stress, renal failure, acute heart failure, hypotension, obesity,	
CC	anorexia, HIV infections, osteoporosis, angina pectoris, and myocardial	
CC	infarction. (I) and (II) are useful for modulating signal transduction	
CC	activity. (I) and (II) are useful as an inhibitor of chemotaxis, as a	
CC	food additive or preservative, and for modifying the activities of (I).	
CC	(I) and (II) also useful to modulate mammalian characteristics, such as	
CC	body height, weight, hair color, eye color, skin, percentage of adipose	
CC	tissue, pigmentation, size and shape, to change a mammal's mental state	
CC	or physical state by influencing biorhythms, caracaid rhythms,	
CC	depression, tendency for violence, tolerance for pain, reproductive	
CC	capabilities, hormonal or endocrine levels, appetite, libido, memory,	
CC	stress, or other cognitive qualities. This sequence corresponds to the	
CC	coding sequence for the novel HGPRBMY30 protein.	
XX		

SQ	Sequence 3446 BP; 594 A; 1171 C; 1083 G; 598 T; 0 U; 0 Other;	
	Query Match 58.6%; Score 2086.2; DB 10; Length 3446;	
	Best Local Similarity 81.8%; Pred. No. 0;	
	Matches 2744; Conservative 0; Mismatches 3; Indels 606; Gaps 5;	
QY	211 ATGCTGGGCCCCTGCTGCTGGGCTCAGCCTCTGGGCTCTCTGACCCCTGGGACGGG 270	
Db		
	1 ATGCTGGGCCCCTACAGTCTGGGCTCAGCCTCTGGGCTCTCTGACCCCTGGGACGGG 60	
QY	271 GCCCAATTGTGCTGTCAAGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGCTG 330	
Db		
	61 GCCCAATTGTGCTGTCAAGCAACTTAGGATGAAGGGGACTACGTGCTGGGGGGCTG 120	
QY	331 TTCCCTGGGCGAGGCGGAGGCTGGGCTCCGACGCGGACACGGCCAGCCT 390	
Db		
	121 TTCCCTGGGCGAGGCGGAGGCTGGGCTCCGACGCGGACACGGCCC----- 171	
QY	391 GTGTGACCAAGGTACAGAGGTGGGACGCTTGGGTCTGGGTCTAGGGGTACCAAGTCTGGG 450	
Db	-----	171
QY	451 GTGCTCTGAGCTGGGCGGAGGTGGCCATCTCGGTTCTGTGTGGCCCCCAGGTTCTCCT 510	
Db		
	172 -----CCATCTCGGTTCTGTGTGGCCCCCAGGTTCTCCT 205	
QY	511 CAAACGGCTGCTCTGGGCACTGGCCATGAAATGGCCGTGGAGAGATCAACAACAGT 570	
Db		
	206 CAAACGGCTGCTCTGGGCACTGGCCATGAAATGGCCGTGGAGAGATCAACAACAGT 265	
QY	571 CGGATCTGCTGCGGGCTGCGCTGGGCTACGACCTCTTTGATACGTGCTCGGAGCCTG 630	
Db		
	266 CGGATCTGCTGCGGGCTGCGCTGGGCTACGACCTCTTTGATACGTGCTCGGAGCCTG 325	
QY	631 TGGTGGCCATGAAGCCAGCCTCATGTTCTGGCCAAAGGAGGAGCGCGGACATCGCCG 690	
Db		
	326 TGGTGGCCATGAAGCCAGCCTCATGTTCTGGCCAAAGGAGGAGCGCGGACATCGCCG 385	
QY	691 CCTACTGCACTACAGCAGTACCAGCCCGTGTGCTGGTGTCTATCGGGCCCCACTCGT 750	
Db		
	386 CCTACTGCACTACAGCAGTACCAGCCCGTGTGCTGGTGTCTATCGGGCCCCACTCGT 445	
QY	751 CAGAGCTCGCATGCTCACCAGCAAGTTCTTCAGCTTCTTCTCATGCCCGCAGTGGGGCG 810	
Db		
	446 CAGAGCTCGCATGCTCACCAGCAAGTTCTTCAGCTTCTTCTCATGCCC----- 495	
QY	811 CCCCCCAACCATACCCACCCCCCAACCCCTGCCCCGTGGGAGCCCTTGTGTCAAGGA 870	
Db	-----	495
QY	871 GAATGCTACATGCACCCCAACCCAGCCCTGCCCTGGGAGCCCTGTGTCAAGATGCTCTT 930	
Db	-----	495
QY	931 GGCCTTGCAAGTACAGTACGGTGTAGCATGAGCTGTGAGCGCCCGGAGACCTTCCC 990	
Db		
	496 -----CAGGTACGTACGGTGTAGCATGAGCTGTGAGCGCCCGGAGACCTTCCC 548	
QY	991 CTCCTTCTTCCGCAAGTCCCAGCGACCGTGTGAGCTGACGGCCGCCCGGAGCTGCT 1050	
Db		
	549 CTCCTTCTTCCGCAAGTCCCAGCGACCGTGTGAGCTGACGGCCGCCCGGAGCTGCT 608	
QY	1051 GCAGGAGTTCGGCTGGAACCTGGGTGGCCCGCTGGGAGCGGACGACGAGTACGGCCGCA 1110	
Db		
	609 GCAGGAGTTCGGCTGGAACCTGGGTGGCCCGCTGGGAGCGGACGACGAGTACGGCCGCA 668	
QY	1111 GGGCCTGAGCATCTTCTCGGCCCTGGCCCGGCAACGCGCATCTGTCATCGCGCAGAGGG 1170	
Db		
	669 GGGCCTGAGCATCTTCTCGGCCCTGGCCCGGCAACGCGCATCTGTCATCGCGCAGAGGG 728	
QY	1171 CTGGTCCCGCTGCCCGTGCATGACTCGCGGCTGGGAAAGGTGCAGGACGTCTGCA 1230	
Db		
	729 CTGGTCCCGCTGCCCGTGCATGACTCGCGGCTGGGAAAGGTGCAGGACGTCTGCA 788	

QY	1231 CCAGGTGAACCCAGAGCAGCGTGCAGGTGGTGTGCTGTGTTTCCGCTCCGTGCACGCCGCCCA 1290	
Db		
	789 CCAGGTGAACCCAGAGCAGCGTGCAGGTGGTGTGCTGTGTTTCCGCTCCGTGCACGCCGCCCA 848	
QY	1291 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCAAAGGTGTGGTGGCCAGCGA 1350	
Db		
	849 CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCAAAGGTGTGGTGGCCAGCGA 908	
QY	1351 GGCCTGGCTGACCTCTGACCTGGTTCATGGGGCTGCCCGCATGGCCAGATGGGCACGGT 1410	
Db		
	909 GGCCTGGCTGACCTCTGACCTGGTTCATGGGGCTGCCCGCATGGCCAGATGGGCACGGT 968	
QY	1411 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACGAGTTCCTCCAGTACCTGTAAGACGCA 1470	
Db		
	969 GCTTGGCTTCTCCAGAGGGGTGCCAGCTGCACGAGTTCCTCCAGTACCTGTAAGACGCA 1028	
QY	1471 CCTGGCCCTGGCCACCGACCCGGCTTCTGCTCTGCTGGGGGAGAGGGAGCAGGTTCT 1530	
Db		
	1029 CCTGGCCCTGGCCACCGACCCGGCTTCTGCTCTGCTGGGGGAGAGGGAGCAGGTTCT 1088	
QY	1531 GGAGAGGACGTGGTGGCCAGCGCTGCCCGCAGTGTACTGTCATCAGTGCAGAACGT 1590	
Db		
	1089 GGAGAGGACGTGGTGGCCAGCGCTGCCCGCAGTGTACTGTCATCAGTGCAGAACGT 1148	
QY	1591 GAGCGAGGGCTAAATCACCAACAGACGTTCTTCTGTCTACGAGCTGTGTATAGCTGGC 1650	
Db		
	1149 GAGCGAGGGCTAAATCACCAACAGACGTTCTTCTGTCTACGAGCTGTGTATAGCTGGC 1208	
QY	1651 CCAGGCCCTGCACAACTCTTCACTGCAACGCTCAGGCTGCCCGCAGGACCCCGT 1710	
Db		
	1209 CCAGGCCCTGCACAACTCTTCACTGCAACGCTCAGGCTGCCCGCAGGACCCCGT 1268	
QY	1711 GAAGCCCTGGCAGGTGAGCCCGGAGATGGGGTGTGCTGTCTCTGTCATGTGCCAGGC 1770	
Db		
	1269 GAAGCCCTG----- 1277	
QY	1771 CACGAGGACGGCCACACGCTGAGTGGAGGTGGTGGGGCTCAGCCCCGTCCCCCG 1830	
Db	-----	1277
QY	1831 CCGCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGGGGGCTGCCGTGCG 1890	
Db		
	1278 ---GCAGTCTCTGGAGAACATGTACAACCTGACCTTCCACGTGGGGGGCTGCCGTGCG 1334	
QY	1891 GTTCGACAGCAGCGGAAACGTTGACATGAGTACGACCTGAAGCTGTGGTGTGGCAGGG 1950	
Db		
	1335 GTTCGACAGCAGCGGAAACGTTGACATGAGTACGACCTGAAGCTGTGGTGTGGCAGGG 1394	
QY	1951 CTCAGTCCCAGGCTCCACGACGTGGGAGGTTCAACGGCAGCTTCAAGCAGAGCGCCT 2010	
Db		
	1395 CTCAGTCCCAGGCTCCACGACGTGGGAGGTTCAACGGCAGCTTCAAGCAGAGCGCCT 1454	
QY	2011 GAAGATCCGTGGCACACGTCTGACAAACAGGTGAGGTGAGGTGGGTGTGCCAGGCGTG 2070	
Db		
	1455 GAAGATCCGTGGCACACGTCTGACAAACAGGT----- 1487	
QY	2071 CCCGTGGTAGCCCCCGCGGACGGCGCAGCTGGGGGTGGGGCGGTTCCAGTCTCCCGT 2130	
Db	-----	1487
QY	2131 GGGCATGCCAGCCAGCAGAGCAGAGCCAGACCCAGGCTGTGCGCAGAAAGCCCGTGTCCCG 2190	
Db		
	1488 -----GCCGTGTCCCGG 1500	
QY	2191 TGCTCGCGGACGTGCCAGGAGGGCCAGGTGCGCGGGTCAAGGGGTTCCACTCTGCTGC 2250	
Db		
	1501 TGCTCGCGGACGTGCCAGGAGGGCCAGGTGCGCGGGTCAAGGGGTTCCACTCTGCTGC 1560	
QY	2251 TACGACTGTGTGGACTGCGAGGGGGCAGCTACCGGCAAAACCCAGGTGAGCGCGCTTCC 2310	
Db		
	1561 TACGACTGTGTGGACTGCGAGGGGGCAGCTACCGGCAAAACCC----- 1603	

QY 2311 CGGACGGCGGGGTGGGAACGCAGCAGGGGAGGGTCCTGCCAAGTCTGACTCTGAGACC 2370
Db 1604 ----- 1603
QY 2371 AGAGCCACAGGGTACAAGACGAACACCCAGCGCCCTTCTCCTCTCTCACAGACGACATC 2430
Db 1604 -----CAGACGACATC 1614
QY 2431 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGGAAGACACGCTGCTTCCGC 2490
Db 1615 GCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGGAAGACACGCTGCTTCCGC 1674
QY 2491 CGCAGGTCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGCTGCTGCTGCTGCTGCTG 2550
Db 1675 CGCAGGTCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGCTGCTGCTGCTGCTGCTG 1734
QY 2551 AGCCTGGCGCTGGGCCCTTGTGCTGGCTGCTTTGGGGCTGTTTCGTTCAACCATCGGACAGC 2610
Db 1735 AGCCTGGCGCTGGGCCCTTGTGCTGGCTGCTTTGGGGCTGTTTCGTTCAACCATCGGACAGC 1794
QY 2611 CCACGTGTTCAGGCCCTCGGGGGGGCCCTGGCCCTGCTTTTGGCTGGTGTGCTGGCCCTG 2670
Db 1795 CCACGTGTTCAGGCCCTCGGGGGGGCCCTGGCCCTGCTTTGGCCCTGGTGTGCTGGCCCTG 1854
QY 2671 GTCGCTCAGCGTCTCCTCTGTTCCCTGGCCAGCCCCAGCCCTGCCGATGCCCTGGCCCCAG 2730
Db 1855 GTCGCTCAGCGTCTCCTCTGTTCCCTGGCCAGCCCCAGCCCTGCCGATGCCCTGGCCCCAG 1914
QY 2731 CAGCCCTGTGCCACCTCCCGCTACGGGCTGCCTGAGCACACTTCTTCTGTCAGGCGGCC 2790
Db 1915 CAGCCCTGTGCCACCTCCCGCTACGGGCTGCCTGAGCACACTTCTTCTGTCAGGCGGCC 1974
QY 2791 GAGATCTTCGTGGAGTCAGAACTGCCTCTGAGCTGGGCAGACCCGGCTGAGTGGCTGCCCTG 2850
Db 1975 GAGATCTTCGTGGAGTCAGAACTGCCTCTGAGCTGGGCAGACCCGGCTGAGTGGCTGCCCTG 2034
QY 2851 CGGGGGCCCTGGGCCCTGGCTGGTGGTGGCTGCTGGCCATGCTGTGGAGGTGCACTGTGC 2910
Db 2035 CGGGGGCCCTGGGCCCTGGCTGGTGGTGGCTGCTGGCCATGCTGTGGAGGTGCACTGTGC 2094
QY 2911 ACCTGTFACCTGGTGGCCCTTCCCGCGGAGGTGGTGACGGACTGGCACATGTCGCCACG 2970
Db 2095 ACCTGTFACCTGGTGGCCCTTCCCGCGGAGGTGGTGACGGACTGGCACATGTCGCCACG 2154
QY 2971 GAGGCGCTGGTGCACTGCCGCACACGCTCCTGGGTGAGCTTCGGCCTAGCGCACGCCACC 3030
Db 2155 GAGGCGCTGGTGCACTGCCGCACACGCTCCTGGGTGAGCTTCGGCCTAGCGCACGCCACC 2214
QY 3031 AATGCCACGCTGGCCCTTCTCTGCTTCTTCTGGGCACCTTTCCTGTTGCGGAGCCAGCCGGGC 3090
Db 2215 AATGCCACGCTGGCCCTTCTCTGCTTCTTCTGGGCACCTTTCCTGTTGCGGAGCCAGCCGGGC 2274
QY 3091 TGCTACAACCGTGCCCGTGGCCCTCACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTC 3150
Db 2275 CGCTACAACCGTGCCCGTGGCCCTCACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTC 2334
QY 3151 TCCTTTGTGCCCCCTCCTGGCCAAATGTGCAGGTGGTCCCTCAGGCCCGCCGTCAGATGGGC 3210
Db 2335 TCCTTTGTGCCCCCTCCTGGCCAAATGTGCAGGTGGTCCCTCAGGCCCGCCGTCAGATGGGC 2394
QY 3211 GCCCTCTGCTCTGTGCTCTGGCAATCCTGGCTGCTTCCACCTGCCAGGTGTTACCTG 3270
Db 2395 GCCCTCTGCTCTGTGCTCTGGCAATCCTGGCTGCTTCCACCTGCCAGGTGTTACCTG 2454
QY 3271 CTCATGGCGCAGCCAGGGCTCAACACCCCGAGTTCTTCTTGGAGGGGGCCCTGGGGAT 3330
Db 2455 CTCATGGCGCAGCCAGGGCTCAACACCCCGAGTTCTTCTTGGAGGGGGCCCTGGGGAT 2514
QY 3331 GCCCAAGCCAGAAATGACGGGAACACAGGAAATCAGGGGAACATGAGTGACCCAAACCT 3390
Db 2515 GCCCAAGCCAGAAATGACGGGAACACAGGAAATCAGGGGAACATGAGTGACCCAAACCT 2574
QY 3391 GTGATCTCAGCCCCCGGTGAACCCAGACTTAGCTGCGATCCCCCCCCAAGCCAGCAATGACC 3450

Db 2575 GTGATCTCAGCCCCGGTGAAACCAGACTTAGCTGCGATCCCCCCCAAGCCAGCAATGACC 2634
QY 3451 CGTGTCTCGCTACAGAGACCCCTCCGCTCTAGGTTCTGACCCAGGTTGTCTCTGACCC 3510
Db 2635 CGTGTCTCGCTACAGAGACCCCTCCGCTCTAGGTTCTGACCCAGGTTGTCTCTGACCC 2694
QY 3511 TGACCCACAGTGAGCCCTAGGCTGGAGCACGTGGACACCCCTGTGACCATC 3563
Db 2695 TGACCCACAGTGAGCCCTAGGCTGGAGCACGTGGACACCCCTGTGACCATC 2747
RESULT 13
AAL38462
ID AAL38462 standard; cDNA; 3458 BP.
XX AAL38462;
AC AAL38462;
XX
DT 15-AUG-2002 (first entry)
XX
DE cDNA encoding a human G-protein coupled receptor (GPCR).
XX
KW G-protein coupled receptor; GPCR; gene chip; human; immune response;
KW chromosomal position; transgenic animal; gene therapy; gene; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 30..2588
FT /*tag= a
FT /product= "Human G-protein coupled receptor"
XX
PN WO200230981-A1.
XX
PD 18-APR-2002.
XX
PF 13-MAR-2001; 2001WO-US007832.
XX
PR 10-OCT-2000; 2000US-00684393.
XX
PA (PEXE) PE CORP NY.
XX
PI Wei M, Zhong W, Ketchum KA, Difrancesco V, Beasley EM;
XX
DR WPI; 2002-444173/47.
DR P-PSDB; AAO21501.
XX
PT Novel G protein coupled receptor, useful for raising antibodies, to
PT elicit immune response, and as a reagent in assays designed to
PT quantitatively determine levels of protein in biological samples.
XX
PS Claim 1; Fig 1; 82pp; English.
XX
CC The invention relates to an isolated G-protein coupled receptor (GPCR)
CC polypeptide, comprising an 852 residue amino acid sequence, given in the
CC specification, an allelic variant or ortholog of the protein, or a
CC fragment comprising at least 10 contiguous amino acids of the protein.
CC GPCR is useful for identifying a modulator of GPCR and an agent that
CC binds to GPCR. GPCR and a gene chip comprising GPCR are useful as models
CC for the development of human therapeutic agents. GPCR is useful for
CC raising antibodies, to elicit immune response, as a reagent in assays
CC designed to quantitatively determine levels of protein in biological
CC samples, and as markers for tissues in which the corresponding protein is
CC preferentially expressed. A gene chip containing GPCR is also useful as a
CC probe for determining the chromosomal positions of nucleic acid molecules
CC by means of in situ hybridisation, in making vectors containing the gene
CC regulatory regions of a gene chip containing GPCR, for designing
CC ribozymes, in making vectors that express GPCR, and for constructing host
CC cells and transgenic animals expressing nucleic acid molecules and
CC peptides. A host cell containing GPCR is useful for conducting cell-based
CC assays involving GPCR protein or its fragments, and for identifying
CC protein mutants in which these function is affected. The polynucleotide
CC encoding GPCR can be used to treat disorders by gene therapy. This

QY 2248 TGCTACGACTGTGTGGACTCGAGGGCGGCAGCTACCGGCAAAACCCAGGTGAGCCGCCT 2307
Db 1581 TGCTACGACTGTGTGGACTCGAGGGCGGCAGCTACCGGCAAAACC----- 1626
QY 2308 TCCCGGCAGGCGGGGTGGAAACGCAGCAGGGGAGGGTCTTGCCAAAGTCCTGACTCTGAG 2367
Db 1627 ----- 1626
QY 2368 ACCAGAGCCCAAGGGTACAAGACGAACACCCAGCGCCCTTCTCCTCTCTCACAGACGAC 2427
Db 1627 -----CAGACGAC 1634
QY 2428 ATGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACACGCTGCTTC 2487
Db 1635 ATGCCTGCACCTTTTGTGGCCAGGATGAGTGGTCCCGGAGCGAAGCACACGCTGCTTC 1694
QY 2488 CGCCGCAAGTCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGCTGCTGCTCTCTGCTG 2547
Db 1695 CGCCGCAAGTCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGCTGCTGCTCTCTGCTG 1754
QY 2548 CTGAGCCTGGCGTGGCCCTTGTGCTGCTGCTTTTGGGGCTGTTCTGTTACCATCGGGAC 2607
Db 1755 CTGAGCCTGGCGTGGCCCTTGTGCTGCTGCTTTTGGGGCTGTTCTGTTACCATCGGGAC 1814
QY 2608 AGCCCACTGTTTACGGCCTCGGGGGGGCCCTGGCCTGCTTTGGCCTGGTGTGCCTGGG 2667
Db 1815 AGCCCACTGTTTACGGCCTCGGGGGGGCCCTGGCCTGCTTTGGCCTGGTGTGCCTGGG 1874
QY 2668 CTGGTCTGCTCAGCGTCTCTGTTCCCTGCTCAGCGGCTGCCAGCCCTGCCCCGATGCCTGGC 2727
Db 1875 CTGGTCTGCTCAGCGTCTCTGTTCCCTGCTGCGGCTGCCAGCCCTGCCCCGATGCCTGGC 1934
QY 2728 CAGCAGCCTTGTCCACCTCCCGCTCAGCGGCTGCCAGCACACTTCTCTGACGGCG 2787
Db 1935 CAGCAGCCTTGTCCACCTCCCGCTCAGCGGCTGCCAGCACACTTCTCTGACGGCG 1994
QY 2788 GCCGAGATCTTCGTGGAGTCAGAACTGCCTCTGAGCTGGGCGAGACCGGCTGAGTGGCTGC 2847
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QY 2968 ACGGAGCGCTGGTGCACTGCCGACACGCTCCTGGGTGAGTGGTGGCTAGCGCACGCC 3027
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QY 3028 ACCAATGCCACGCTGGCCTTCTCTGCTTCTGGGCACCTTCTGGGTGCGGAGCCAGCCG 3087
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QY 3088 GGCTGCTACAACCGTGGCGCTGACCTTTCATGCTGGCTTCTGCTGCTGCTGCTGCTGCTG 3147
Db 2295 GGCGCTACAACCGTGGCGCTGACCTTTCATGCTGGCTTCTGCTGCTGCTGCTGCTGCTG 2354
QY 3148 GTCTCCTTTGTGCCCCCTCCTGGCAATGTGAGGTGGTCTGAGGCGCCCGCTGAGATG 3207
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Db 2415 GGCGCCTCCTGCTGCTGCTGGGCATCCTGGTGGCTTCCACCTGCCAGGTGTAC 2474
QY 3268 CTGCTCATGCGGAGCCAGGCTCAACACCCCGAGTTCCTTCTGGAGGGGCGCCCTGGG 3327
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QY 3328 GATCCCCAAGCCAGAAATGACGGGAACACAGGAAATCAGGGGAACATGAGTGACCCAAAC 3387
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QY 3448 ACCCGTGTCTCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCAGGTTGTCTCTGA 3507
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Db 2715 CCCTGACCCACAGTGAGCCCTAGGCTGGAGCACGTGGACACCCCTGTGACCCATC 2770
RESULT 15
ABL55952
ID ABL55952 standard; cDNA; 2729 BP.
XX
AC ABL55952;
XX
DT 17-JUN-2002 (first entry)
XX
DE Human G-protein coupled receptor encoding cDNA SEQ ID NO 12.
XX
KW Human; GPCR; G-protein coupled receptor; receptor; anti-HIV; antitumour;
KW antiinflammatory; antiallergic; antianaemic; antiasthmatic; virucide;
KW immunosuppressive; dermatological; nephrotropic; antigout; antithyroid;
KW cytostatic; neuroprotective; osteopathic; antipsoriatic; antirheumatic;
KW antiarthritic; thyromimetic; antiulcer; ophthalmological; antibacterial;
KW fungicide; antiparasitic; protozoacide; antihelminthic; antidiabetic;
KW antiarteriosclerotic; hepatotropic; anticonvulsant; anorectic; metabolic;
KW antiemetic; antidiarrhoeic; neuroleptic; cerebroprotective; nootropic;
KW antiparkinsonian; depilatory; tranquilizer; hypotensive; vasotropic;
KW cardiant; antianal; vulnary; proliferative disorder; cancer;
KW neurological disorder; Alzheimer's disease; Huntington's disease;
KW Parkinson's disease; multiple sclerosis; meningitis; prion;
KW cardiovascular disorder; acquired immunodeficiency syndrome; AIDS;
KW Crohn's disease; diabetes mellitus; rheumatoid arthritis; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2592
FT /*tag= a
FT /product= "G-protein coupled receptor"
XX
WO200198323-A2.
27-DEC-2001.
15-JUN-2001; 2001WO-US019354.
16-JUN-2000; 2000US-0212483P.
23-JUN-2000; 2000US-0213950P.
26-JUN-2000; 2000US-0214062P.
07-JUL-2000; 2000US-0216595P.
14-JUL-2000; 2000US-0218936P.
19-JUL-2000; 2000US-0219154P.
XX
(INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Graul R, Hafalia AJA, Walia NK, Thornton M, Nguyen DB;
PI Lu Y, Gandhi AR, Patterson C, Kallilck DA, Baughn MR, Ramkumar J;
PI Tribouley CM, Lee EA, Ding L, Burford N, Yao MG, Yang J;
PI Griffin JA;
XX
DR WPI; 2002-139780/18.
DR P-PSDB; ABB77318.
XX
PT Novel G-protein coupled receptor protein and polynucleotides useful for

diagnosing, treating or preventing disorders of cell proliferation e.g. cancer, neurological and genetic disorder e.g. thalassemia.

Claim 48; Page 116-117; 121pp; English.

The invention relates to a G-protein coupled receptor protein (GCREC) polypeptide (ABB77317-ABB77326). The GCREC is useful for screening an agonist/antagonist of GCREC, a compound that specifically binds to GCREC or that modulates the activity of GCREC. GCREC is also useful as an immunogen for preparing antibodies which are useful for diagnosing a condition of disease associated with expression of GCREC in a subject, for detecting and purifying GCREC from a sample. The GCREC encoding polynucleotide (ABL55951-ABL55960) is useful for screening for a compound effective in altering expression of GCREC. GCREC is also useful for assessing toxicity of a test compound useful for treating a disease or condition associated with decreased expression or overexpression of functional GCREC. Examples of disorders include cell proliferative disorder such as arteriosclerosis, atherosclerosis, hepatitis, mixed connective tissue disease (MCTD), psoriasis and cancer including adenocarcinoma, leukaemia; a neurological disorder such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease, retinitis pigmentosa, multiple sclerosis, bacterial and viral meningitis, abscess, subdural empyema; prion disease including kuru, Creutzfeldt-Jakob disease; fatal familial insomnia, neurofibromatosis, tuberous sclerosis, cerebral palsy, polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; seasonal affective disorder (SAD); akathisia, and amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, Tourette's disorder; cardiovascular disorders such as hypertension, vasculitis, vascular tumours, congestive heart failure, ischaemic heart disease, myocardial infarction, calcific aortic valve stenosis, infective endocarditis, endocarditis of systemic lupus erythematosus, cardiac transplantation; gastrointestinal disorder such as dysphagia, gastritis, anorexia, nausea, emesis, abdominal angina, infections of the intestinal tract, peptic ulcer, hepatitis, cirrhosis, diarrhoea, acquired immunodeficiency syndrome (AIDS) enteropathy, jaundice, Reye's syndrome, liver infarction; an autoimmune/inflammatory disorder such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, psoriasis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a metabolic disorders such as diabetes, obesity, and osteoporosis. The GCREC encoding polynucleotide is useful for gene therapy and for creating knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease

QY	451	GTGCTCCTGAGCTGGGCGGAGGTGGCCATCTGCGGTTCTGTGTGGCCCCCAGGTTCTCCT	510
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QY	571	CGGATCTGCTGCCCGGCTGCGCTGGGCTACGACCTCTTTGATACGTGCTCGGAGCCTG	630
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Db	320	TGGTGGCCATGAAGCCAGCCTCATGTTCTTGGCCAAAGGCAGGCGCGGACATCGCCG	379
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Db	440	CAGAGCTCGCCATGGTCAACGGCAAGTTCTTCAGCTTCTTCTCATGCCCC-----	489
QY	811	CCCCCCCACCAACCCACCCCAACCAACCCCTGCCCCCGTGGGAGCCCCCTGTGTCAAGGA	870
Db	490	-----	489
QY	871	GAATGCTACATGCACCCCAACCCAGCCCTGCCCCTGGGAGCCCTGTGTCAAGATGCTCTT	930
Db	490	-----	489
QY	931	GGCCTTGCAAGTCAGCTACGGTGTCTAGCATGGAGCTGCTGAGCGGCCCGGAGACCTTCCC	990
Db	490	-----CAGGTCAGCTACGGTGTCTAGCATGGAGCTGCTGAGCGGCCCGGAGACCTTCCC	542
QY	991	CTCCTTCTTCCGACACCGTGTCCCAGCGACCGGTGTGACGTGACGCGGCCCGCGGAGCTGCT	1050
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QY	1111	GGGCCTGAGCATCTTCTCGGCCCTTGGCCGCGGACCGCGCATCTGCATCGCGCACGAGGG	1170
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QY	1171	CCTGGTGCCGCTGCCCGTGCATGACTCGGGCTGGGAAGGTGCAGSACGTCTCTGCA	1230
Db	723	CCTGGTGCCGCTGCCCGTGCATGACTCGGGCTGGGAAGGTGCAGSACGTCTCTGCA	782
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QY	1291	CGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGGA	1350
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QY	1351	GGCCTGGCTGACCTCTGACCTGGTTCATGGGGTGCCTGGCATGGCCCCAGATGGGCACGGT	1410
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QY 1591 GAGCGCAGGGCTAAATCACCACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTGGC 1650
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QY 1711 GAAGCCCCTGGCAGGTGAGCCCGGGAGATGGGGGTGTGCTGTCTCTGCAATGTGCCCCAGGC 1770
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Db 1588 TACGACTGTGTGACTGCGAGCGGGCAGCTACCGGCAAAACC----- 1630
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Db 1882 GTCTGCCCTCAGGTCCTCCTGTTCCCTGGCCAGCCCCAGCCCTGCCCGATGCCCTGGCCCCAG 1941
QY 2731 CAGCCCCTGTCCACACCTCCCGCTCACCGGGCTGCTGAGCACACTCTTCTCTGCAGGCGGCC 2790
Db 1942 CAGCCCCTGTCCACACCTCCCGCTCACCGGGCTGCTGAGCACACTCTTCTCTGCAGGCGGCC 2001
QY 2791 GAGATCTTCGTGGAGTCAGAACTGCCCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCCTG 2850
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GenCore version 5.1.6
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Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	663	18.6	684	5	BX117730
C 2	366.4	10.3	750	5	BQ178590
C 3	288	8.1	495	4	BM706305
C 4	219.2	6.2	323	2	AW417577
C 5	187.8	5.3	830	8	AZ750699
C 6	154.8	4.3	168	1	AA907022
C 7	153	4.3	210	9	CE644804
C 8	151.4	4.2	558	2	BE754542
C 9	130.6	3.7	2373	9	AY410649
C 10	124.2	3.5	2376	9	AY410651
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C 14	101.8	2.9	1038	9	CNS0506R
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C 16	93	2.6	3115	3	AK029770
C 17	90.4	2.5	2738	3	AK077434
C 18	87	2.4	938	4	BI462667
C 19	81	2.3	525	9	CC546019
C 20	77.4	2.2	612	4	BM439858
C 21	77.2	2.2	1041	9	CNS01ZX1
C 22	75.6	2.1	829	9	CNS04565
C 23	74.6	2.1	641	6	CA426652
C 24	74	2.1	718	8	AZ972907

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C 26	71.6	2.0	699	7	CN218468
C 27	71	2.0	703	7	CO043387
C 28	70.8	2.0	2182	3	AK034263
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C 30	69.8	2.0	498	2	AW051287
C 31	69.2	1.9	525	8	AZ483105
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C 37	68.6	1.9	877	9	CG141385
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C 39	67.4	1.9	1244	4	BG846745
C 40	67	1.9	562	1	AI742401
C 41	66.6	1.9	925	9	CNS0091P
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ALIGNMENTS

RESULT 1
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DEFINITION BX117730 Soares_NFL_T GBC_S1 Homo sapiens CDNA clone
IMAGp9981153811 ; IMAGE:1505750, mRNA sequence.
ACCESSION BX117730
VERSION BX117730.1 GI:27881047
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp9981153811.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAACAGCTATGAC.

FEATURES
source

Location/Qualifiers
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/note="Organ: pooled; Vector: pR773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCL-CPAP-GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

	Query Match	18.6%;	Score 663;	DB 5;	Length 684;
	Best Local Similarity	98.2%;	Pred. No. 5.8e-119;		
	Matches 663;	Conservative	0;	Mismatches 12;	Indels 0; Gaps 0;
QY	1693	CCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCCGGGAGATGGGGGTGTGCTGTC			
Db	675	CCCCGCNCAGGACNCCGTNAAGCCCTGGCAGGTGAGNCCGGNANATGGGGGTGNTCTGTC			
QY	1753	CTCTGCATGTGCCAGGCCACACAGGCACGGCCACCAACGCTGAGCTGAGGTGGCTGGCG			
Db	615	CTNTGCATGTGCCAGGCCNNCAGGCNCGGCCNCCACGCTGAGCTGAGGTGGCTGGCG			
QY	1813	GCTCAGCCCCGTCCCGCCCGCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGT			
Db	555	GCTCAGCCCCGTCCCGCCCGCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGT			
QY	1873	GGCGGGCTGCCGCTGCGTTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAA			
Db	495	GGCGGGCTGCCGCTGCGTTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAA			
QY	1933	GCTGTGGTGTGGCAGGCTCAGTGCCCGCAGGCTCCACGACGTGGGCAGGTTCAACGGCAG			
Db	435	GCTGTGGTGTGGCAGGCTCAGTGCCCGCAGGCTCCACGACGTGGGCAGGTTCAACGGCAG			
QY	1993	CCTCAGGACAGAGCGCCTGAAGATCCGCTGSCACACGCTTGACAAACAGGTGAGGTGAGG			
Db	375	CCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGCTTGACAAACAGGTGAGGTGAGG			
QY	2053	GTGGGTGTGCCAGGCGTCCCGTGGTAGCCCCCGGCAGGCGCAGCCTGGGGTGGGG			
Db	315	GTGGGTGTGCCAGGCGTCCCGTGGTAGCCCCCGGCAGGCGCAGCCTGGGGTGGGG			
QY	2113	GCCGTTCCAGTCTCCCGTGGGCATGCCCCAGCCGAGCAGAGCCAGACCCCGCCTGTGCG			
Db	255	GCCGTTCCAGTCTCCCGTGGGCATGCCCCAGCCGAGCAGAGCCAGACCCCGCCTGTGCG			
QY	2173	CAGAAAGCCCGTGTCCCGGTGCTCCGCGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAG			
Db	195	CAGAAAGCCCGTGTCCCGGTGCTCCGCGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAG			
QY	2233	GGGTTCCACTCCTGCTGCTACGACTGTGTGGA CTGCGAGCGCGGCAGCTACCGGCAAAAC			
Db	135	GGGTTCCACTCCTGCTGCTACGACTGTGTGGA CTGCGAGCGCGGCAGCTACCGGCAAAAC			
QY	2293	CCAGGTGAGCCGCTTCCCGGCAGCGGGGGTGGGAACGACAGGGGAGGTCCTGCCA			
Db	75	CCAGGTGAGCCGCTTCCCGGCAGCGGGGGTGGGAACGACAGGGGAGGTCCTGCCA			
QY	2353	AGTCCTGACTCTGAG 2367			
Db	15	AGTCCTGACTCTGAG 1			

RESULT 2

LOCUS	BQ178590	750 bp	mRNA	linear	EST 30-APR-2002
DEFINITION	UI-M-EV0-bws-h-23-0-UI.r1 NIH_BMAP_EVO Mus musculus cDNA clone				
	IMAGE:5701318 5', mRNA sequence.				
ACCESSION	BQ178590				
VERSION	BQ178590.1	GI:20354082			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

Db 304 TTTAGTTACAGCATCCATCATGGCCCTCTACCCCAAGGTATGGTGGCCAGTGAGTCTTGG 245
QY 1358 CTGACCTCTGACCTGGTCTATGGGGCTGCGCGCATGGCCAGATGGGCACGGTGTCTTGGC 1417
Db 244 CTGACATCTGACCTGGTCTATGACACTTCCCAATATTGCCCGTGGGCACTGTCTTGGG 185
QY 1418 TTCCTCCAGAGGGGTGCCAGCTGCAGAGTTCCTCCAGTACGTGAAGACGCACCTGGCC 1477
Db 184 TTTTTCAGCGGGGTGCCCTACTGCTGTAATTTTCCCATATTATGTGAGACTCACCTTGGC 125
QY 1478 CTGGCCACCGACCCGGCCTTCTGCTCTGCTGCTGGCGGAGAGGAGGAGGCTCTGGAGGAG 1537
Db 124 CTGGCGCTGACCCAGCATTTCTGTGCTCACTG---AATGCGAGTTGGATCTGGAGGAA 68
QY 1538 GACGTGGTGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGTGCAGAAACGTGAGCGCA 1597
Db 67 CATGTGATGGGGCAACGCTGTCCACGGTGTGACGACATCATGCTGCAGAACCTATCATCT 8
QY 1598 GGGCT 1602
Db 7 GGGCT 3

RESULT 3
BM706305
LOCUS
DEFINITION
UI-E-DW0-agh-a-22-0-UI.r1 495 bp mRNA linear EST 28-FEB-2002
UI-E-DW0-agh-a-22-0-UI 5', mRNA sequence.
BM706305
BM706305.1 GI:19019563
EST.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hagenan
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. .495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DW0-agh-a-22-0-UI"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DW0 is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an

FEATURES
source

oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CGATTAGCGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
ORIGIN
Query Match 8.1%; Score 288; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 9.9e-46;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3276 GCGGCAGCCAGGGCTCAACACACCCCGAGTTCTTCTGGAGGGGGCCCTGGGGATGCCCA 3335
Db 1 GCGGCAGCCAGGGCTCAACACACCCCGAGTTCTTCTGGAGGGGGCCCTGGGGATGCCCA 60
QY 3336 AGCCAGAAATGACGGGAACACAGGAAATCAGGGGAACATGAGTACCCAAACCCCTGTAT 3395
Db 61 AGCCAGAAATGACGGGAACACAGGAAATCAGGGGAACATGAGTACCCAAACCCCTGTAT 120
QY 3396 CTCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCCCAAGCCAGCAATGACCCGTGT 3455
Db 121 CTCAGCCCCGGTGAACCCAGACTTAGCTGCGATCCCCCAAGCCAGCAATGACCCGTGT 180
QY 3456 CTCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCAGGTTGTCTCCTGACCCCTGACC 3515
Db 181 CTCGCTACAGAGACCCCTCCCGCTCTAGGTTCTGACCCAGGTTGTCTCCTGACCCCTGACC 240
QY 3516 CCACAGTGAGCCCTAGGCTGGAGCACGTCGGACACCCCTGTGACCATC 3563
Db 241 CCACAGTGAGCCCTAGGCTGGAGCACGTCGGACACCCCTGTGACCATC 288

RESULT 4
AW417577
LOCUS
DEFINITION
54413 MARC 1PIG Sus scrofa cDNA 5', mRNA linear EST 09-JUL-2000
AW417577
VERSION
AW417577.1 GI:6945459
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 323)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Perteau,G., Sultana,R.,
Quackenbush,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 20 row: E column: 14
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. .323
/organism="Sus scrofa"

FEATURES
source

ORIGIN

Query Match 6.2%; Score 219.2; DB 2; Length 323;
Best Local Similarity 82.3%; Pred. No. 2.6e-32;
Matches 251; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

19 GGACTGGCGTGGCTACCCACANAGGCACTGGTGCACTGCCGCTGCACTCCTGGATCAG 78

2949 GGACTGGCACATGCTGCCACGGAGCGCTGGTGCACTGCCGACACAGCTCCTGGGTGAG 3008

3009 CTTGGGCTAGCGACGCCACCAATGCCACGCTGGCCTTTCTCTGCTTCTGGGCACTTT 3068

79 CTTGAGCCTGGTACATGCTGCCAATGCCACGCTGGCTTCTCTGCTTCTGGGCACTTT 138

3069 CCTGGTGGGAGCCAGCGGGCTGCTACAACCGTGCCGCTGGGCTCCTGCTTTGCCATGCT 3128

139 CTTGGTGACAGCCAGCCTGGTACCAACACAGGGGGCGAGCCTGACCTTCGCCATGCT 198

3129 GGCCTACTTCACTACCTGGTCTCTTTGTGCCCCCTCCTGGCCAAATGTGCAAGTGGTCT 3188

199 GGCCTACTTCACTACCTGGTCTCTTTGTGCCCCCTCCTAGCCAACGTGCTGGGCTC 258

3189 CAGGCCGCGGTGACATGGGGCCCTCCTGCTGTGCTCTGGGCATCCTGGCTGCTTT 3248

259 CCAGCTGCGGTGACATGGGTGCGGCCCTCCTCTGTGTGCTGGGCATCCTGGCCACTTT 318

3249 CCACC 3253

319 CCACC 323

FEATURES

source

Location/Qualifiers

1. .830

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-112J8"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; The RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN

Query Match 5.3%; Score 187.8; DB 8; Length 830;
Best Local Similarity 58.5%; Pred. No. 3.8e-26;
Matches 430; Conservative 0; Mismatches 257; Indels 48; Gaps 4;

1579 GCTGCAGAACGTGAGCGCAGGGCTAAATCACACACAGAGCTTCTCTGTCTACGCAGCTGT 1638

43 GTTGCAAGAACCTATCAGCTGGGCAATTGCACCAATAATTTGCAACCTATGCACTGT 102

1639 GTATAGCGTGGCCAGGCCCTGCACAACACTCTTTAGTGCAACGCCTCAGGCTGCCCGC 1698

103 GTACAGTGTGGCTCAAGCCCTTCAACAACCCCTACAGTGAATGTCTCATTGCCAGT 162

1699 GCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGGGGTGTGTCTCTGCTGC 1758

163 ATCAGAACATGTTTACCTTGGCAGGTAAAGGTAGGGTTTGTGCTGGGTTTTC---C 218

1759 ATGTGCCCCAGGCCACAGGCGCCACCAACGCTGAGCTGGAGGTGGCTG--GCGGCTC 1816

219 TGCTCCTGCAGGAACACTGAACACAGGCCAGCCAAATCTTGTGTGACTGGAGAGGCCT 278

1817 AGCCCGTCCCCCGCGAGCTCTCTGGAGAACATGTACAACCTGACCTTCCACGTGGGC 1876

279 TACCTGACTCCACTCCACAGCTCTGGAGAACATGTACAATATGATTTCCATGCTCGA 338

1877 GGGTGTCCCGTGGTTCGACAGCAGCGGAAACGCTGGACATGGAGTACGACCTGAAGCTG 1936

339 GACTTGACACTACAGTTTGTATGCTGAAGGGAATGTAGACATGGAATATGACCTGAAGATG 398

1937 TGGTGTGGCAGGGCTCAGTCCGAGGCTCCACGACGTGGGAGGTTTCAACGGCAGCCTC 1996

399 TGGGTGTGGCAGAGCCCTACACCTGTATTACATACTGTGGGCACTTCAACGGCACCCCT 458

1997 AGGACAGAGCGCCTGAAGATCCGCTGGCACACGCTCTGACAACAGGTTGAGGTGAGGTGG 2056

459 CAGCTGCAGCAGTCTAAATGTACTGGC-----CAGGCAACCAAGTAAGGACAAGACAG 512

2057 GTGTGCCAGGGCTGCCCCGTGGTAGCCCCCGGCGCAGGGCGCAGCTGGGGTGGGGCCG 2116

513 GCAAAAGGATGGTGGTAGAAGCTTGTGGTCTTGGGCCAGTGTAGCCAAAGGGG--- 568

2117 TTCCAGTCTCCCGTGGGCATGCCACGCGAGCAGCCAGACCCAGGCTGTGCGCAGA 2176

569 -----AGGCCTAACCCAGGCTCCATGTACAGG 596

2177 AGCCCGTGTCCCGTGTCTCGCGGAGTGGCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGT 2236

597 TGCCAGTCTCCAGTGTTCGCCCGCAGTGAAGATGGCCAGGTTCCCGGAGTAAGGGCT 656

2237 TCCACTCCTGCTGCTACGACTGTGTGGAGTGGCGAGCGGGCAGTACCGGCAAAACCCAG 2296

657 TTCAATTCCTGCTGCTATGACTGCGTGGAGTGAAGGCGGGCAGTACCGGGAGCATTCAG 716

2297 GTGAGCCGCTTCCC 2311

717 GTGAACCGTCTTCC 731

RESULT 5

AZ750699

LOCUS

DEFINITION

830 bp DNA linear GSS 25-JAN-2001

RPCI-24-112J8.TV RPCI-24 Mus musculus genomic clone RPCI-24-112J8,

genomic survey sequence.

ACCESSION

AZ750699

VERSION

AZ750699.1 GI:12535858

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 830)

Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,

Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other_GSSs: RPCI-24-112J8.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 112 row: J column: 8

Seq primer: T7

Class: BAC ends.

RESULT 6
AA907022
LOCUS
DEFINITION
Oj92a08.s2 Soares NFL_T GBC_S1 Homo sapiens cDNA clone
IMAGE:1505750 3', mRNA sequence.
ACCESSION
AA907022.1 GI:3042482
VERSION
AA907022
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 168)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 825 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 157.
FEATURES
source
1..168
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1505750"
/lab_host="DH10B"
/clone_lib="Soares NFL_T GBC_S1"
/note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. Clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 4.3%; Score 154.8; DB 1; Length 168;
Best Local Similarity 98.7%; Pred. No. 9.3e-20;
Matches 156; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1619 TTCTCTGTCTACGAGTGTGTATAGCGTGGCCCGCCAGCCCTGCACAACACTCTTCAGTGC 1678
|||
Db 11 TTTTGTGTCTACGAGTGTGTATAGCGTGGCCCGCCAGCCCTGCACAACACTCTTCAGTGC 70
QY 1679 AACGCCTCAGGCTGCCCGCGCAGGACCCCGTGAGCCCTGGCAGGTGAGCCCGGAGAT 1738
|||
Db 71 AACGCCTCAGGCTGCCCGCGCAGGACCCCGTGAGCCCTGGCAGGTGAGCCCGGAGAT 130
QY 1739 GGGGGTGTGCTGCTCTGTCATGTGCCCGCCAGCCACCAG 1776
|||
Db 131 GGGGGTGTGCTGCTCTGTCATGTGCCCGCCAGCCACCAG 168
RESULT 7
CE644804
LOCUS
DEFINITION
tigr-gss-dog-1700367133648 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION
CE644804
VERSION
CE644804.1 GI:36963644
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)

ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 210)
AUTHORS
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
TITLE
The dog genome: survey sequencing and comparative analysis
JOURNAL
Science 301 (5641), 1898-1903 (2003)
MEDLINE
22875432
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..210
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 4.3%; Score 153; DB 9; Length 210;
Best Local Similarity 83.3%; Pred. No. 2.1e-19;
Matches 174; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 3010 TTCGGCCTAGCGACGCCACCAATGCCACGCTGGCCTTCTCTGTTCTTCTGGCACTTTC 3069
|||
Db 1 TTTGGCCTAGTGCATGCCATCAATGCCATGCTGGCCTTCTCTGTTCTTCTGGCACTTTC 60
QY 3070 CTGGTGGGAGCCAGCGGGCTGCTACAACCGTGGCCGTGGCCTCACCTTTGCCATGCTG 3129
|||
Db 61 TTGGGGCAGAGCCGGCCAGCGCGCTACAATGGCGCCGGGTCTCACCTTTGCCATGCTG 120
QY 3130 GCCTACTTCATCACCCTGGGTCTCCTTTGTGCCCTCCTGGCCAATGTGCAGTGGTCTC 3189
|||
Db 121 GCCTACTTCATCACCCTGGATCTCCTTTGTCCCTCTCTTTGCCAATGTGCATGTGCCTAC 180
QY 3190 AGGCCCGCGCTGCAGATGGCGCCCTCCT 3218
|||
Db 181 CAGCCCACTGTGCAGATGGCGCCCACTCCT 209
RESULT 8
BE754542
LOCUS
DEFINITION
208082 MARC 2BOV Bos taurus cDNA 5', mRNA linear
ACCESSION
BE754542
VERSION
BE754542.1 GI:10168534
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 558)
AUTHORS
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
Genome Res. 11 (4), 626-630 (2001)
MEDLINE
21180013

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:663147
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyt not found
 High quality sequence stop: 286.

FEATURES

source
 1. .298
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1260595"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse heart (#937316)"
 /note="Organ: heart; Vector: pBluescript SK-; Site 1: ECORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 2.9%; Score 103.4; DB 1; Length 298;
 Best Local Similarity 63.5%; Pred. No. 1.1e-09;
 Matches 158; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
 QY 938 CAGGTCAGCTACGGTGTCTAGCATGGAGCTGTGAGCGCCCGGAGACCTTCCCTCCTTC 997
 Db |||||
 QY 295 CAGGTCAGCTATGAGCGGAGCAGCGTGATCCTCAGTGGGAAGCGCAAGTTCCCGTCCTTC 236
 Db |||||
 QY 998 TTCCGACACCGTGCCCGAGCGACCGTGTGACAGCTGACGGCGCGCGGAGCTGTGCAGGAG 1057
 Db |||||
 QY 235 TTGCGCACCATCCCCAGCGATAAGTACCAGGTGGAAGTCATAGTCCGGTGTGCAGAGC 176
 QY 1058 TTCCGCTGGAACCTGGGTGGCGCGCTGGGCGAGCGACGACGAGTACGGCGGCGGCTG 1117
 Db |||||
 QY 175 TTCCGCTGGGTCTGGATCTCGTCTGGCAGCTATGTTGACTACGGGCGAGTGGCGTA 116
 QY 1118 AGCATCTTCTCGGCCCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1177
 Db |||||
 QY 115 CAGGCGCTGGAGGAGCTGGCCACTCCACGGGCGATCTGCGTCCGCTTCAAGGACGTGGTG 56
 QY 1178 CCGCTGCC 1186
 Db |||||
 55 CCTCTCTCC 47

RESULT 14

CNS0506R/c
 LOCUS
 DEFINITION
 Tetraodon nigroviridis genome survey sequence T7 end of clone
 006M17 of library B from Tetraodon nigroviridis, genomic survey sequence.
 AL315180
 AL315180.1 GI:9548068
 GSS; genome survey sequence.
 SOURCE
 Tetraodon nigroviridis
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
 REFERENCE
 1
 AUTHORS
 Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
 TITLE
 Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

Nat. Genet. 25 (2), 235-238 (2000)
 20296633
 10835645
 2

Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

10899143

3 (bases 1 to 1038)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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; Sequence 20, Application US/09799629
; Publication No. US20030008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
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; SEQ ID NO 20
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-629-20
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; Publication No. US20030054448A1
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; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035,045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
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QY 1621 CTCTGTCTACGAGCTGTGTATAGCTGGCCAGGCCCTGCACAAACTCTTCAAGTCAA 1680
Db 1621 CTCTGTCTACGAGCTGTGTATAGCTGGCCAGGCCCTGCACAAACTCTTCAAGTCAA 1680
QY 1681 CGCCTCAGGCTGCCCGCAGGACCCCGTGAAGCCCTGAGCCCTGGCAGGTGAGCCCGGAGATGG 1740
Db 1681 CGCCTCAGGCTGCCCGCAGGACCCCGTGAAGCCCTGAGCCCTGGCAGGTGAGCCCGGAGATGG 1740
QY 1741 GGGTGTGCTGTCTCTGATGTGCCCCAGGCCACAGGCACGGCCACCGCTGAGCTGG 1800
Db 1741 GGGTGTGCTGTCTCTGATGTGCCCCAGGCCACAGGCACGGCCACCGCTGAGCTGG 1800
QY 1801 AGGTGGCTGGCGCTCAGCCCCGTCCCCCGCCGCTCAGGAGAACATGTACAACTT 1860
Db 1801 AGGTGGCTGGCGCTCAGCCCCGTCCCCCGCCGCTCAGGAGAACATGTACAACTT 1860
QY 1861 GACCTTCCAGTGGGCGGCTGCCGTGCGGTTGACAGCAGCGGAAACGTGGACATGGA 1920
Db 1861 GACCTTCCAGTGGGCGGCTGCCGTGCGGTTGACAGCAGCGGAAACGTGGACATGGA 1920
QY 1921 GTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCACAGGCTCCACGACGTGGGCAG 1980
Db 1921 GTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCACAGGCTCCACGACGTGGGCAG 1980
QY 1981 GTTCAAACGGCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGTCTGACAAACA 2040
Db 1981 GTTCAAACGGCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGTCTGACAAACA 2040
QY 2041 GGTGAGGTGAGGGTGGTGTGCCAGGCGTGCCTGTGAGCCCGCGGCGGCGCAGC 2100
Db 2041 GGTGAGGTGAGGGTGGTGTGCCAGGCGTGCCTGTGAGCCCGCGGCGGCGCAGC 2100
QY 2101 CTGGGGGTGGGGCCGTTCCAGTCTCCCGTGGGCATGCCAGCCGAGCAGAGCCAGCCC 2160
Db 2101 CTGGGGGTGGGGCCGTTCCAGTCTCCCGTGGGCATGCCAGCCGAGCAGAGCCAGCCC 2160
QY 2161 CAGGCTGTGCGCAGAAAGCCCGTGTCCCGTGTCTCGGCGAGTCCAGGAGGGCCAGGTG 2220
Db 2161 CAGGCTGTGCGCAGAAAGCCCGTGTCCCGTGTCTCGGCGAGTCCAGGAGGGCCAGGTG 2220
QY 2221 CGCGGGGTCAAGGGGTTCCACTCTGCTACGACTGTGTGGAATGCGAGCGGGCAGC 2280
Db 2221 CGCGGGGTCAAGGGGTTCCACTCTGCTACGACTGTGTGGAATGCGAGCGGGCAGC 2280
QY 2281 TACCGCAAAACCCAGGTGAGCCGCTTCCCGGAGGCGGGGTGGAAACGACAGGGG 2340
Db 2281 TACCGCAAAACCCAGGTGAGCCGCTTCCCGGAGGCGGGGTGGAAACGACAGGGG 2340
QY 2341 AGGTCCTGCCAAGTCTGACTCTGAGACCGAGCCACAGGTTACAGACGAACACCCA 2400
Db 2341 AGGTCCTGCCAAGTCTGACTCTGAGACCGAGCCACAGGTTACAGACGAACACCCA 2400
QY 2401 GCGCCCTTCTCTCTCAACAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGG 2460
Db 2401 GCGCCCTTCTCTCTCAACAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGAGTGG 2460

QY 2461 TCCCCGGAGCGAAGCACACAGCTGCTTCCGCCGCGAGGTCTCGGTTCTCGCATGGGGCGAG 2520
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2461 TCCCCGGAGCGAAGCACACAGCTGCTTCCGCCGCGAGGTCTCGGTTCTCGCATGGGGCGAG 2520
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2521 CCGGCTGTGCTGCTGCTCCTGCTGCTGAGCCCTGGCGCTGGGCCCTTGTGCTGGCTGCT 2580
QY 2581 TTGGGGCTGTTCTGTTACCATCGGGACAGCCCACTGGTTAGGCCCTCGGGGGGGCCCCCTG 2640
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2581 TTGGGGCTGTTCTGTTACCATCGGGACAGCCCACTGGTTAGGCCCTCGGGGGGGCCCCCTG 2640
QY 2641 GCCTGCTTTGGCCCTGGTGTGCCTGGGCCCTGGTCTGCCTCAGCGTCTCCTGTTCCTTGGC 2700
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2641 GCCTGCTTTGGCCCTGGTGTGCCTGGGCCCTGGTCTGCCTCAGCGTCTCCTGTTCCTTGGC 2700
QY 2701 CAGCCCAGCCCTGCCGATGCCCTGGCCCCAGAGCCCTTGTCCCACCTCCCGTCAACGGGC 2760
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2701 CAGCCCAGCCCTGCCGATGCCCTGGCCCCAGAGCCCTTGTCCCACCTCCCGTCAACGGGC 2760
QY 2761 TGCCTGAGCACACTTCTCTGCAGGCGGCGGAGATCTTCTGTGAGTCAGAACTGCCTCTG 2820
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2821 AGCTGGGCAGACCGGCTGAGTGGCTGCCCTGCGGGGCCCCCTGGGCTGGCTGGTGGTCTG 2880
QY 2881 CTGGCCATGCTGGTGGAGTGCACACTGTGCACCTGGTACCTGGTGGCTTCCCGCCGGAG 2940
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2881 CTGGCCATGCTGGTGGAGTGCACACTGTGCACCTGGTACCTGGTGGCTTCCCGCCGGAG 2940
QY 2941 GTGGTGACGGACTGGCACATGCTGCCCCACGGAGCGCTGGTGCACTGCCGACACAGCTCC 3000
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2941 GTGGTGACGGACTGGCACATGCTGCCCCACGGAGCGCTGGTGCACTGCCGACACAGCTCC 3000
QY 3001 TGGGTGAGTTCGGGCTAGCGCACGCCACCAATGCGACGCTGGCCTTTCTCTGCTTCCTG 3060
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3001 TGGGTGAGTTCGGGCTAGCGCACGCCACCAATGCGACGCTGGCCTTTCTCTGCTTCCTG 3060
QY 3061 GGCACCTTTCCTGGTGGGAGCCAGCCGGGCTGTACAACCGTGCCCGTGGCCTCACCTTT 3120
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3061 GGCACCTTTCCTGGTGGGAGCCAGCCGGGCTGTACAACCGTGCCCGTGGCCTCACCTTT 3120
QY 3121 GCCATGCTGGCCCTACTTCATCACCTGGGTCTCCTTTGTGCCCTCCTGGCCAATGTGCGAG 3180
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3121 GCCATGCTGGCCCTACTTCATCACCTGGGTCTCCTTTGTGCCCTCCTGGCCAATGTGCGAG 3180
QY 3181 GTGGTCTTCAGGCCCGCGTGCAGATGGGCGCCCTCTGCTCTGTGTCCTGGGCATCCTG 3240
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3181 GTGGTCTTCAGGCCCGCGTGCAGATGGGCGCCCTCTGCTCTGTGTCCTGGGCATCCTG 3240
QY 3241 GCTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGCGGCGAGCCAGGGCTCAACACCCCC 3300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3241 GCTGCCTTCCACCTGCCAGGTGTTACCTGCTCATGCGGCGAGCCAGGGCTCAACACCCCC 3300
QY 3301 GAGTTCCTTCAGGGGGGGCCCTGGGGATGCCAAGGCCAGAAATGACGGGAACACAGGA 3360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3301 GAGTTCCTTCAGGGGGGGCCCTGGGGATGCCAAGGCCAGAAATGACGGGAACACAGGA 3360
QY 3361 AATCAGGGGAAACATGAGTGACCCAACTGTGATCTCAGCCCCGGTGAACCCAGACTTA 3420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3361 AATCAGGGGAAACATGAGTGACCCAACTGTGATCTCAGCCCCGGTGAACCCAGACTTA 3420
QY 3421 GCTGCGATCCCCCCCCAAGCCAGCAATGACCCCGTGTCTGCTACAGAGACCCCTCCCGCTCT 3480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3421 GCTGCGATCCCCCCCCAAGCCAGCAATGACCCCGTGTCTGCTACAGAGACCCCTCCCGCTCT 3480
QY 3481 AGGTTCTGACCCCCAGGTTGTCTCCTGACCCCTGACCCCAAGTACAGTGGCCCTGAGC 3540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3481 AGGTTCTGACCCCCAGGTTGTCTCCTGACCCCTGACCCCAAGTACAGTGGCCCTGAGC 3540
QY 3541 ACGTGGACACCCCTGTGACCATC 3563

Db 3541 ACGTGGACACCCCTGTGACCATC 3563
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RESULT 3
US-10-725-081-20
; Sequence 20, Application US/10725081
; Publication No. US20040132075A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/10/725,081
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 30/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-725-081-20

Query Match 100.0%; Score 3563; DB 17; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGGCCGAGGAGCGA 60
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1 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGGCCGAGGAGCGA 60
QY 61 GGACACCACCTGGGGCCCCAGGGTGTGGCAAGTGGAGATGGCAAGGTTTGTCTAAACAAA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 GGACACCACCTGGGGCCCCAGGGTGTGGCAAGTGGAGATGGCAAGGTTTGTCTAAACAAA 120
QY 121 TCCTCTGCCCGTCCCCCGCCCCGGGCTACTCCATGTGAGGCCCCAGTGGGGCAGCCAC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 TCCTCTGCCCGTCCCCCGCCCCGGGCTACTCCATGTGAGGCCCCAGTGGGGCAGCCAC 180
QY 181 CTGCCGTGCCTGTGGAAAGTTGCCTCTGCCATGTGGGCCCTGTCTCTGGGCCTCAGC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 CTGCCGTGCCTGTGGAAAGTTGCCTCTGCCATGTGGGCCCTGTCTCTGGGCCTCAGC 240
QY 241 CTCTGGGCTCTCTGTCACCCCTGGACCGGGGCCCCCATTTGGCTGTCAAGCAACTTAGG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTCTGGGCTCTCTGTCACCCCTGGACCGGGGCCCCCATTTGGCTGTCAAGCAACTTAGG 300
QY 301 ATGAAGGGGGACTACGTGTGGGGGGGGTGTTCCTCCCTGGGCGAGGCCGAGGAGGCTGGC 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 ATGAAGGGGGACTACGTGTGGGGGGGGTGTTCCTCCCTGGGCGAGGCCGAGGAGGCTGGC 360
QY 361 CTCGCGACCGGACACGGCCCCAGCCCTGTGTGCA CCAGGTACAGAGGTGGGACGGCC 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CTCGCGACCGGACACGGCCCCAGCCCTGTGTGCA CCAGGTACAGAGGTGGGACGGCC 420
QY 421 TGGGTGCGGGTCAGGGTGACCCAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCCAT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TGGGTGCGGGTCAGGGTGACCCAGGTCTGGGGTGTCTCTGAGCTGGGGCCGAGGTGGCCAT 480

QY 481 CTGCGGTTCTGTGTGGCCCCAGGTTCTCCTCAAACGGCCTGCTCTGGGCACTGGCCATGA 540
Db |||||
QY 541 AAATGGCCGTGGAGGAGATCAACAACAAGTCGGATCTGCTGCCGGCTGCGCCTGGGCT 600
Db |||||
QY 601 ACGACCTCTTTGATACGTCTCGGAGCCTGTGGTGGCCATGAAGCCAGCCTCATGTTCC 660
Db |||||
QY 661 TGGCCAAGGCAGGCAGCCGCGACATCGCCGCCCTACTGCAACTACACGCAGTACCGACCCC 720
Db |||||
QY 721 GTGTGCTGGCTGTCTATCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCCGGCAAGTTCT 780
Db |||||
QY 781 TCAGCTTCTTCTCCTCATGCCCCAGTGGGGGCCCCCACCACCATCACCCACCCCCAACCAACC 840
Db |||||
QY 841 CCTGCCCCGTGGGAGCCCTTGTGTCAAGAGAAATGCTACAGATGATGCTACAGGTACGCTACGCTGCTAGCAT 900
Db |||||
QY 901 CCTGGAGCCCTGTGTCAAGAGATGCTCTTGGCCCTTGAGGTACGCTACGCTACGCTGCTAGCAT 960
Db |||||
QY 961 GGAGCTGCTGAGCGCCCGGAGACCTTCCCCCTCCTTCTCCGCACCGTGCCTCAGGACCG 1020
Db |||||
QY 1021 TGTGACGTGACCGGCCCGCGGAGCTGCTGCAGGAGTTCGGCTGGAACCTGGGTGGCCGC 1080
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QY 1081 CCTGGGCAGCGACGAGTACGGCCGGCAGGGCCCTGAGCATCTTCTCGGCCCTGGCCGC 1140
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QY 1141 GGCACGCGGCATCTGCAATCGCGCACGAGGGCCTGGTGGCCGTGCCCCGTGCCGATGACTC 1200
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QY 1201 GCGGCTGGGGAAGGTGCAAGAGCTCTTGCAACAGGTGAACACAGAGCAGCGTGCAAGTGGT 1260
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QY 1261 GCTGCTGTTCCGCTCCGTGCAAGAGCTGCTGCGGCTGCCCCGTGCCGATGACTC 1320
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QY 1321 GCTCTCGCCCAAGGTGCGGTCAGCGAGGCTGGCTGACCTCTGACCTGGTCAATGGG 1380
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QY 1381 GCTGCCCCGATGGGCCAGTGGGCACGGTCTTGGCTTCTCCAGAGGGGTGCCAGCT 1440
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QY 1441 GCACGAGTTCCTCCAGTACGTGAAGACGCACCTGGCCCTGGCCACCGACCCGGCCTTCTG 1500
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QY 1501 CTCTGCCCTGGCGAGAGGAGCAGGGTCTGGAGGAGACGTGGTGGGCCAGCGCTGCC 1560
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QY 1561 GCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGAGGGCTAAATCACCAACGAGCTT 1620
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QY 1621 CTCTGTCTACGCAGCTGTGTATAGCGTGGCCAGGCCCTGCACAACACTCTTTCAGTGCAA 1680
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QY 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCCTGAAGCCCTGGCAGGTGAGCCCCGGGAGATGG 1740
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QY 1741 GGGTGTGCTGTCTCTGTCATGTGCCAGGCCACAGGCACGGCCACCAACGCTGAGCTGG 1800
Db |||||
QY 1801 AGGTGGCTGGCGGCTCAGCCCCCGTCCCCCGCGGAGCTCTTGAGAAACATGTACAACCT 1860
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QY 1861 GACCTTCCACGTGGCGGCTGCCGCTGCCGTTGACAGCAGCGGAAACGTGGACATGGA 1920
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QY 1921 GTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGTCCCAGGCTCCACGACGTGGCAG 1980
Db |||||
QY 1981 GTTCAAACGGCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGCTCTGACAACCA 2040
Db |||||
QY 2041 GGTGAGGTGAGGGTGTGCCAGGCGTCCCCTGAGTCCCGTGGTACCCCCCGGGCAGCGCAGC 2100
Db |||||
QY 2101 CTGGGGTGGGGCCGTTCCAGTCTCCCCTGGGCATGCCACGCGAGCAGACGACCCC 2160
Db |||||
QY 2161 CAGGCCTGTGCGCAGAACCCGTGTCCCCTGCGGCTGCGCGGAGTCCAGGAGGGCCAGGTG 2220
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QY 2221 CGCCGGGTCAAGGGTTCCACTCCTGTGCTACGACTGTGTGACTGCGAGGCGGCGAGC 2280
Db |||||
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QY 2521 CCGGCTGTGCTGCTGCTCCTGTGCTGAGCCTGCGCTGGGCCCTTGTGCTGGCTGCT 2580
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Db 2701 CAGCCAGCCCTGCCGATGCTGGCCAGCAGCCCTTGTGCCACCTCCCGCTACGGGC 2760
QY 2761 TGCCTGAGCACACTCTTCCTGAGCGCGCCGAGATCTTCGTGAGTCAGAACTGCCTCTG 2820
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Db 2881 CTGGCCATGCTGGTGGAGTGCACCTGTGACCTGGTACCTGGTGGCTTCCCGCCGGAG 2940
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QY 3001 TGGGTACGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTGGCTTCTGCTTCCCTG 3060
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QY 3061 GGCACCTTTCCTGGTGGGAGCCAGCCGGCTGTACAAACCGTGCCGCTGGCCTCACCTTT 3120
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QY 3121 GCCATGCTGGCTACTTTCATCACCTGGTGGTCTCTTGTGCCCCCTCTGGCCCAATGTGAG 3180
Db 3121 GCCATGCTGGCTACTTTCATCACCTGGTGGTCTCTTGTGCCCCCTCTGGCCCAATGTGAG 3180
QY 3181 GTGGTCTCAGGCCCGCGTGAGATGGGGCCCTCCTGCTGTGTCTGGGCACTCCTG 3240
Db 3181 GTGGTCTCAGGCCCGCGTGAGATGGGGCCCTCCTGCTGTGTCTGGGCACTCCTG 3240
QY 3241 GCTGCTTCCACCTGCCAGGTGTTACCTGCTCATGCGGAGCCAGGGCTCAACACCCCC 3300
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QY 3361 AATCAGGGGAAACATGAGTGACCCCAACCTGTGATCTCAGCCCCGGTGAAACCCAGACTTA 3420
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Db 3541 ACGTGGACACCCCTGTGACCATC 3563

RESULT 4
US-10-724-223-20
; Sequence 20, Application US/10724223
; Publication No. US20040171042A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/10/724,223
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 30/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-223-20

Query Match 100.0%; Score 3563; DB 17; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGCCCCAGGAAGCGA 60
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QY 61 GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGGAGATGGCAAGGTTTGTCTAAACAAA 120
Db 61 GGACACCACTGGGGCCCCAGGGTGTGGCAAGTGGAGATGGCAAGGTTTGTCTAAACAAA 120
QY 121 TCCTCTGCCCGTCCCGCCCGGCTCACTCCATGTGAGGCCCCAGTGGGGCTCAGC 180
Db 121 TCCTCTGCCCGTCCCGCCCGGCTCACTCCATGTGAGGCCCCAGTGGGGCTCAGC 180
QY 181 CTGCCGTGCTTGGAAAGTTGCCTCTGCCATGTGGGCCCTGCTGTCTGGGCTCAGC 240
Db 181 CTGCCGTGCTTGGAAAGTTGCCTCTGCCATGTGGGCCCTGCTGTCTGGGCTCAGC 240
QY 241 CTCTGGGCTCTCTGCACCCCTGGGACCGGGGCCCTTGTGCCTGTACAGCAACTTAGG 300
Db 241 CTCTGGGCTCTCTGCACCCCTGGGACCGGGGCCCTTGTGCCTGTACAGCAACTTAGG 300
QY 301 ATGAAGGGGACTACGTGTGGGGGGCTGTTCCTCCCTGGGCGAGCCGAGGAGGCTGGC 360
Db 301 ATGAAGGGGACTACGTGTGGGGGGCTGTTCCTCCCTGGGCGAGCCGAGGAGGCTGGC 360
QY 361 CTCCGCAGCCGACACGGCCCGCAGCCCTGTGTGACCCAGGTACAGAGTGGGACGGCC 420
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Db 421 TGGGTGGGGTCAAGGTGACCCAGGTCTGGGGTGTCTGAGCTGGGGCTGAGGCTGGCCAT 480
QY 481 CTGGGTTCTGTGGGGGGCTTCTCCTCAACGGCCCTGCTCTGGGGCTGAGGCTGGCCATGA 540
Db 481 CTGGGTTCTGTGGGGGGCTTCTCCTCAACGGCCCTGCTCTGGGGCTGAGGCTGGCCATGA 540
QY 541 AAATGGCCGTGGAGAGATCAACAAAGTGGATCTGTGCCGGCTGCGGCTGGGCT 600
Db 541 AAATGGCCGTGGAGAGATCAACAAAGTGGATCTGTGCCGGCTGCGGCTGGGCT 600
QY 601 ACGACCTCTTTGATACGTCTCGGAGCCCTGTGGTGGCCATGAAGCCCGATGTTCC 660
Db 601 ACGACCTCTTTGATACGTCTCGGAGCCCTGTGGTGGCCATGAAGCCCGATGTTCC 660

QY 661 TGGCAAGGCAGGCAGCCGCGACATCGCCGCCTACTGCAACTACAGCAGTACCAGCCCC 720
Db 661 TGGCAAGGCAGGCAGCCGCGACATCGCCGCCTACTGCAACTACAGCAGTACCAGCCCC 720
QY 721 GTGTGCTGGCTGTATCGGGCCCCACTCGTCAGAGCTCGGCATGGTCAACGGCAAGTTCT 780
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QY 781 TCAGTTCTTCTCATGCCCCAGTGGGGCGCCCCCACCACATCAACCCCCAACCAACC 840
Db 781 TCAGTTCTTCTCATGCCCCAGTGGGGCGCCCCCACCACATCAACCCCCAACCAACC 840
QY 841 CCTGCCCGCTGGAGCCCTTGTGTACAGAGAAATGCTACATGCACCCCCACCCAGCCCTGC 900
Db 841 CCTGCCCGCTGGAGCCCTTGTGTACAGAGAAATGCTACATGCACCCCCACCCAGCCCTGC 900
QY 901 CCTGGAGCCCTGTGTACAGAGATGCTCTTGGCCCTTGACAGGTACGTAACGGTGTAGCAT 960
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Db 961 GGAGCTGTGAGCGCCCGGGAGACCTTCCCCCTCTTCCGACCCGTGCGGACCG 1020
QY 1021 TGTGACCTGACCGCCCGCGGAGCTGTGCAGAGTTCGGCTGGAATGGGTGGCCGC 1080
Db 1021 TGTGACCTGACCGCCCGCGGAGCTGTGCAGAGTTCGGCTGGAATGGGTGGCCGC 1080
QY 1081 CCTGGGCAGCGACAGTACGGCCGCGAGGCTGTGCAGAGTTCGGCTGGAATGGGTGGCCGC 1140
Db 1081 CCTGGGCAGCGACAGTACGGCCGCGAGGCTGTGCAGAGTTCGGCTGGAATGGGTGGCCGC 1140
QY 1141 GGCAACGGGCATCTGCATCGGCACGAGGCGCTGTGCGCTGCCGATGACTC 1200
Db 1141 GGCAACGGGCATCTGCATCGGCACGAGGCGCTGTGCGCTGCCGATGACTC 1200
QY 1201 GCGGCTGGGAAAGTGCAGGACGTCTTGCACCCAGGTGAACAGAGCAGCGTGCAGGTGGT 1260
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QY 1261 GCTGCTGTTCGCCCTCGGTGCACGCCGCCACGCCCTCTTCAACTACAGCATCAGCAGCAG 1320
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QY 1381 GCTGCCCGCATGGCCCCAGATGGGCACGGTGTGGCTTCTCCAGAGGGTGCCAGCT 1440
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QY 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG 1740
Db 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG 1740
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QY 1861 GACCTTCCACGTGGCGGCTGCGCTGCGGTTTCGACAGCAGCGGAAACGTGGACATGGA 1920
Db 1861 GACCTTCCACGTGGCGGCTGCGCTGCGGTTTCGACAGCAGCGGAAACGTGGACATGGA 1920
QY 1921 GTACGACCTGAAGCTGTGGTGTGGCAGGGCTCAGTGCACAGGCTCCACGACGTGGGCGAG 1980
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Dbb 2821 AGCTGGCAGACCGGCTAGTGGCTGCCTGCGGGGCCCTGGGCTGGCTGGTGGTGGCTG 2880
QY 2881 CTGGCCATGCTGGTGGAGGTGCGACTGTGCACCTGGTACCTGGTGGCCCTTCCCGCCGGAG 2940
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Dbb 3001 TGGGTGAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTGGCCTTTCTGCTTCCTG 3060
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Dbb 3481 AGGTTCTGACCCCGAGTTGTCTCTGACCCCTGACCCCCACAGTGAGCCCTAGGCTGGAGC 3540
QY 3541 ACSTGGACACCCCTGTGACCATC 3563
Dbb 3541 ACSTGGACACCCCTGTGACCATC 3563

RESULT 5

US-10-724-222-20
; Sequence 20, Application US/10724222
; Publication No. US20040191805A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/10/724,222
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/799,629
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-222-20

Query Match 100.0%; Score 3563; DB 18; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dbb 61 GGACACCACCTGGGGCCCCAGSGTGTGGCAAGTGAGGATGGCAAGGGTTTTGCTAAACAAA 120
QY 121 TCCTCTGCCCCCTCCCCGCCCGGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC 180
Dbb 121 TCCTCTGCCCCCTCCCCGCCCGGGGCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCAC 180
QY 181 CTGCCGTGCCTGTTGGAAGTTGCCTCTGCCATGTCTGGGCCCTGCTGTCTGGGCCCTCAGC 240
Dbb 181 CTGCCGTGCCTGTTGGAAGTTGCCTCTGCCATGTCTGGGCCCTGCTGTCTGGGCCCTCAGC 240
QY 241 CTCTGGGCTCTCCTGCACCCCTGGGACGGGGGCCCTGTTCCCCCTGGGCGAGGCCGAGGCTGGC 300
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Dbb 301 ATGAAGGGGGACTACGTGCTGGGGGGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGCTGGC 360
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Dbb 421 TGGGTGCGGGTCAAGGTGACCAAGTCTGGGTGCTCCTGAGCTGGGGCCGAGGTGGCCAT 480
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Dbb 661 TGGCCAAGGCAGGCGCGGACATCGCCGCCCTACTGCAACTACACGCACTACAGGCC 720
QY 721 GTGTGTGGTGTCTATCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGCAAGTTCT 780
Dbb 721 GTGTGTGGTGTCTATCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGCAAGTTCT 780
QY 781 TCAGCTTCTTCTCATGCCCCCAGTGGGGCGCCCCACCACCATCACCCACCCCAACCAACC 840
Dbb 781 TCAGCTTCTTCTCATGCCCCCAGTGGGGCGCCCCACCACCATCACCCACCCCAACCAACC 840

Qy 841 CCTGCCCGTGGAGCCCTTGTGTGTCAGGAGAAATGCTACATGACACCCACCCAGCCCTGC 900
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Qy 901 CCTGGAGCCCTGTGTGTCAGAAATGCTTGGCCCTTGCAGGTACGCTACGGTGTAGCAT 960
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Qy 961 GGAGCTGCTGAGCGCCCGGAGACCTTCCCCTCCTTCTTCCGACCCGTGCCAGCGACCG 1020
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Qy 1021 TGTGAGCTGACCGCCCGCGGAGCTGCTGACGAGTTCCGCTGGAATGGTGGCCCGC 1080
Db |||||
Qy 1081 CCTGGCAGCGACGAGTACCGCCCGGAGGCTGAGCATCTTCTCGGCCCTGGCCCGC 1140
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Qy 1141 GGCACGCGCATCTGCATCGCGCACGAGGCTTGGTCCCGCTGCCGATGACTC 1200
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Qy 1681 CGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGGTGAGCCCGGAGATGG 1740
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Qy 1741 GGGTGTGCTCTCTGTCATGTGCCCCAGGCCACCGGACCGGCCACCGCCTGAGCTGG 1800
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Qy 1861 GACCTTCCAGTGGCGGGCTGCCGTGCGGTCGACAGCAGCGGAACGTTGGACATGGA 1920
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Db 3061 GGCACATTTCCTGGTGGGAGCCAGCCGGCTGTCTACAAACCGTCCCGTGGCCTCACCTTT 3120
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QY 3301 GAGTTCTTCTGGAGGGGCCCTGGGGATGCCCAAGGCCAGATGACGGGAACACAGGA 3360
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Db 3541 ACGTGGACACCCCTGTGACCATC 3563

RESULT 6

US-10-725-276-20
; Sequence 20, Application US/10725276
; Publication No. US20040209286A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/725,276
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-725-276-20

Query Match 100.0%; Score 3563; DB 18; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCTGGCAGTGGCCTCAGGCAGAGTCTGACCGCGCACAACTTTTTCAGGCCCAAGGACGGA 60
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QY 481 CTGGGTTCTGTGGCCCGCAGGTCTCTCAAACGGCCCTGTCTGGGCTGTCGACATGA 540
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Db 3541 ACGTGGACACCCCTGTGACCATC 3563

RESULT 7
US-10-726-568-20
; Sequence 20, Application US/10726568
; Publication No. US20040229239A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/10/726,568
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 30/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-726-568-20

Query Match 100.0%; Score 3563; DB 18; Length 3563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 601
; LENGTH: 4256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(4256)
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; NAME/KEY: CDS
; LOCATION: (201)..(391)
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; NAME/KEY: CDS
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; NAME/KEY: CDS
; LOCATION: (3979)..(4056)
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US-10-292-798-601

Query Match 95.4%; Score 3398.6; DB 15; Length 4256;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 3482; Conservative 0; Mismatches 19; Indels 52; Gaps 2;
QY 11 TGGCCTCAGGCAGAGTCTGACGGCGCACAACTTTCAGGGCCAGGAAGCGAGGACACCACT 70
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Db 61 GGGGCCCCAGGGTGTGGCAAGTAGGATGGCAAGGTTTGTCTAAACAAATCCTCTGCC 120
QY 131 GCTCCCCCGCCCGGCTCACTCCATGTGAGGCCCGCCAGTCGGGGCAGCCACCTGCCGTGCC 190
Db 121 GCTCCCCCGCCCGGCTCACTCCATGTGAGGCCCGCCAGTCGGGGCAGCCACCTGCCGTGCC 180
QY 191 TGTGGAAAGTTGCCCTCTGCCATGCTGGGCCCTGCTGTCCTGGCCCTCAGCCCTCTGGGCTC 250
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QY 251 TCCTGCACCCCTGGGACGGGGCCCCCATTTGTCCTGTACAGCAACTTAGGATGAAGGGGG 310
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QY 311 ACTACGTGCTGGGGGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGTGGCCCTCCGCAGCC 370
Db 301 ACTACGTGCTGGGGGGCTGTTCCCCCTGGGCGAGGCCGAGGAGGTGGCCCTCCGCAGCC 360
QY 371 GGACACGGCCAGAGCCCTGTGTGCACCAAGGTACAGAGGTGGGACGGCCCTGGGTGGGG 430
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QY 431 TCAGGGTGACCAAGTCTGGGGTGTCTGAGCTGGGGCCGAGGTGGCCATCTGCGGTTCT 490
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RESULT 11

US-09-927-315-13

; Sequence 13, Application US/09927315

; Publication No. US20030040045A1

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Ryba, Nicholas J.P.

; APPLICANT: Nelson, Greg

; APPLICANT: Hoon, Mark A.

; APPLICANT: Chandrashekar, Jayaram

; APPLICANT: Zhang, Yifeng

; APPLICANT: The Regents of the University of California

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Mammalian Sweet Taste Receptors

; FILE REFERENCE: 02307E-120110US

; CURRENT APPLICATION NUMBER: US/09/927,315

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: US 60/302,898

; PRIOR FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 3200

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human T1R3 sweet taste receptor genomic

US-09-927-315-13

Query Match 86.7%; Score 3088.2; DB 10; Length 3200;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3182; Conservative 0; Mismatches 18; Indels 53; Gaps 3;

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; LENGTH: 3200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Tlr3 genomic sequence
US-10-190-417-13

Query Match      86.7%; Score 3088.2; DB 15; Length 3200;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3182; Conservative 0; Mismatches 18; Indels 53; Gaps 3;

QY 145 GCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCACCTGCCGTGCCGTGTTGGAAGTTGCC 204
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RESULT 13
US-10-225-567A-592
; Sequence 592, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 592
; LENGTH: 3115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-592
Query Match 83.2%; Score 2965.4; DB 15; Length 3115;
Best Local Similarity 97.6%; Pred. No. 0;
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Db |||||
QY 181 GTGTGCACCAAGGTACAGAGGTGGGAGCGGCTGGCTCCGAGCCGACACGGGTGACAGGTCTGGG 240
Db |||||
QY 451 GTGTCTCTGAGCTGGGCGGAGGTGGGCTGGCTCCGAGCCCTGCTGGGCTTCTGTGGCCCGAGGTCTCCT 510
Db |||||
QY 241 GTGTCTCTGAGCTGGGCGGAGGTGGGCTGGCTCCGAGCCCTGCTGGGCTTCTGTGGCCCGAGGTCTCCT 300
Db |||||
QY 511 CAAACGGCCTGCTCTGGGCACTGGCCATGAAATGCGGCTGGGAGGAGATCAACAAAGT 570
Db |||||
QY 301 CAAACGGCCTGCTCTGGGCACTGGCCATGAAATGCGGCTGGGAGGATCAACAAAGT 360
Db |||||
QY 571 CGGATCTGTGCGCGGCTGGGCTGGGCTACGACCTTCTGATACGTCGTGGGAGCTG 630
Db |||||
QY 361 CGGATCTGTGCGCGGCTGGGCTGGGCTACGACCTTCTGATACGTCGTGGGAGCTG 420
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QY 631 TGGTGGCCATGAAGCCAGCTCATGTTCTTGGCCAGGAGGAGCCGCGACATCGCCG 690
Db |||||
QY 421 TGGTGGCCATGAAGCCAGCTCATGTTCTTGGCCAGGAGGAGCCGCGACATCGCCG 480
Db |||||
QY 691 CCTACTGCAACTACACGCACTACAGCCCTGACAGCCCGTGTGCTGGTGTCTATCGGGGCCCTACTG 750
Db |||||

Db 481 CCTACTGCAACTACAGCAGTACCAGCCCGTGTGCTGGCTGTATCGGCGCCCACTCGT 540
QY 751 CAGAGCTGCCATGGTCAACGGCAAGTTCTTCAGCTTCTTCCATGCCCCAGTGGGGCG 810
Db 541 CAGAGCTGCCATGGTCAACGGCAAGTTCTTCAGCTTCTTCCATGCCCCAG-GTGGCG 599
QY 811 CCCCCCAACATCAACCCACCCCAACCCCTGCCCCGTGGGAGCCCTTGTGTCAAGGA 870
Db 600 CCCCCCAACATCAACCCACCCCAACCCCTGCCCCGTGGGAG---CCCCTGTGTCAAGGA 656
QY 871 GAATGCTACATGCACCCCAACCCAGCCCTGCCCTGGGAGCCCTGTGTCAAGAATGCTCTT 930
Db 657 GATGCT-----CTTG 667
QY 931 GGCCTTGCAAGTCAGCTACGGTGCTAGATGGAGCTGTGAGCGCCGCGGAGACCTTCCC 990
Db 668 GCCCTTGCAAGTCAGCTACGGTGCTAGATGGAGCTGTGAGCGCCGCGGAGACCTTCCC 727
QY 991 CTCCTTCTTCGGCACCGTGCCCCAGCGACCGTGTGCAGCTGACGGCGCCGCGGAGCTGCT 1050
Db 728 CTCCTTCTTCGGCACCGTGCCCCAGCGACCGTGTGCAGCTGACGGCGCCGCGGAGCTGCT 787
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QY 1111 GGGCTGAGCATCTTCTCGGCCCTGGCCGCGGACCGGCAACGAGTACCGGCCGCA 1170
Db 848 GGGCTGAGCATCTTCTCGGCCCTGG-CTCGGCACCGGGCATGTGCATCGCGCACGAGGG 906
QY 1171 CTTGGTCCCGTGCCTCCCGTGCAGTACGCGGCTGGGGAAGGTGCAGGACGTCTGCA 1230
Db 907 CTTGGTCCCGTGCCTCCCGTGCAGTACGCGGCTGGGGAAGGTGCAGGACGTCTGCA 966
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QY 1411 GCTTGGCTTCTCCAGAGGGTGCCAGCTGCACGAGTTCCTCCAGTTCCTCCAGTACGTGAAGACGCA 1470
Db 1147 GCTTGGCTTCTCCAGAGGGTGCCAGCTGCACGAGTTCCTCCAGTTCCTCCAGTACGTGAAGACGCA 1206
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Db 1626 GTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGG 1685
QY 1951 CTCAGTGCCTCAGGCTCCACGACGTGGGAGGTTCAACGGCAGCTCAGGACAGAGCGCT 2010
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Db 2105 AGAGCCACAGGGGACAAAGACGAAACCCAGCGCCCTTCTCCTCTCTCACAGACGACATC 2164
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QY 2491 CGCAGGTCTCGGTCTCTGGCATGGGGCAGCCGGTGTGCTGTGCTCCTGTGCTG 2550
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QY 2851 CGGGGGCCTGGGCTGGCTGGTGGTGTGCTGTGGCCATGCTGGGAGGTGCGACTGTGC 2910
Db 2585 CGGGGGCCTGGGCTGGCTGGTGGTGTGCTGTGGCCATGCTGGGAGGTGCGACTGTGC 2644

QY	2911	ACCTGGTACCTGGTGGCCCTTCCCGCCGGAGTGGTGACGGACTGGCACATGCTGCCACG	2970
DB	2645	ACCTGGTACCTGGTGGCCCTTCCCGCCGGAGTGGTGACGGACTGGCACATGCTGCCACG	2704
QY	2971	GAGGCGCTGGTGCACTGCCGCACACGCTCCTGGGTGAGCTTGGCCCTAGCGCACGCCACC	3030
DB	2705	GAGGCGCTGGTGCACTGCCGCACACGCTCCTGGGTGAGCTTGGCCCTAGCGCACGCCACC	2764
QY	3031	AATGCCACGCTGGCCCTTCTCTGCTTCTCTGGCACTTCTCTGGTGCGGAGCCAGCCGGGC	3090
DB	2765	AATGCCACGCTGGCCCTTCTCTGCTTCTCTGGCACTTCTCTGGTGCGGAGCCAGCCGGGC	2824
QY	3091	TGCTACAAACCGTGCCCGTGGCCCTCACCTTTGCCATGCTGGCCCTACTTCATCACCTGGGTC	3150
DB	2825	CGCTACAAACCGTGCCCGTGGCCCTCACCTTTGCCATGCTGGCCCTACTTCATCACCTGGGTC	2884
QY	3151	TCCTTTGTGCCCTCCTGGCCAATGTGCAGGTGGTCCTCAGGCCCGCCGTCGAGATGGGC	3210
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QY	3211	GCCCTCCTGCTCTGTGTCCTGGGCATCCTGGCTGCCTTCCACCTGCCCAGGTGTACCTG	3270
DB	2945	GCCCTCCTGCTCTGTGTCCTGGGCATCCTGGCTGCCTTCCACCTGCCCAGGTGTACCTG	3004
QY	3271	CTCATGCGGCAGCCAGGCTCAACACCCCGAGTTCTTCTGGGAGGGGCCCTGGGGAT	3330
DB	3005	CTCATGCGGCAGCCAGGCTCAACACCCCGAGTTCTTCTGGGAGGGGCCCTGGGGAT	3064
QY	3331	GCCCAAGGCCAGAAATGACGGGAACACAGGAAATCAGGGGAAACATGAGTGA	3381
DB	3065	GCCCAAGGCCAGAAATGACGGGAACACAGGAAATCAGGGGAAACATGAGTGA	3115

RESULT 14

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US-09-799-629-2
; Sequence 2, Application US/09799629
; Publication No. US20030008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-629-2

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Db	61	GCAGGTACGCTACGGTGTCTAGCATGGAGCTGCTGAGCGCCCGGAGACCTTCCCCTCCTT	120
QY	997	CTTCCGACACCGTGCCCCAGCGACCGTGTGCAGCTGACGGCCCGCGGAGCTGCTGCAGGA	1056
Db	121	CTTCCGACACCGTGCCCCAGCGACCGTGTGCAGCTGACGGCCCGCGGAGCTGCTGCAGGA	180
QY	1057	GTTCGGCTGGAACTGGGTGGCCGCTGGCGCAGCGACGACGACTACGGCCCGCAGGGCCT	1116
Db	181	GTTCGGCTGGAACTGGGTGGCCGCTGGCGCAGCGACGACGACTACGGCCCGCAGGGCCT	240
QY	1117	GAGCATCTTCTCGGCCCTGGCCGCGCACCGGGCATCTGCATCGCGCACGAGGGCCTGGT	1176
Db	241	GAGCATCTTCTCGGCCCTGGCCGCGCACCGGGCATCTGCATCGCGCACGAGGGCCTGGT	300
QY	1177	GCCGCTGCCCGCTGCCGATGACTCGCGCTGGGAAGGTGCAGGACGTCTCTGCACCAGGT	1236
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QY	1237	GAACCAGACGCGTGCAGGTGGTGTCTGCTTTCGCCTCCGTGCACGCCGCCACGCCCT	1296
Db	361	GAACCAGACGCGTGCAGGTGGTGTCTGCTTTCGCCTCCGTGCACGCCGCCACGCCCT	420
QY	1297	CTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCCTG	1356
Db	421	CTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGTGGCCAGCGAGGCCTG	480
QY	1357	GCTGACCTCTGACCTGGTTCATGGGGTGCOCGGCATGGCCAGATGGGACGGTGTCTGG	1416
Db	481	GCTGACCTCTGACCTGGTTCATGGGGTGCOCGGCATGGCCAGATGGGACGGTGTCTGG	540
QY	1417	CTTCCTCCAGAGGGTGCCAGCTGCACGAGTTCCCCAGTACGTGAAGACGCACCTGGC	1476
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QY	1477	CCTGGCCACCGACCCCGCCTTCTGCTCTGCCCTGGCGAGAGGGAGCAGGGTCTGGAGGA	1536
Db	601	CCTGGCCACCGACCCCGCCTTCTGCTCTGCCCTGGCGAGAGGGAGCAGGGTCTGGAGGA	660
QY	1537	GGACGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGC	1596
Db	661	GGACGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGC	720
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QY	1717	CTGGCAGGTGAGCCCCGGGAGATGGGGTGTGCTGTCTCTGCATGTGCCAGGCCACCAG	1776
Db	841	CTGGCAGGTGAGCCCCGGGAGATGGGGTGTGCTGTCTCTGCATGTGCCAGGCCACCAG	900
QY	1777	GCACGGCCACCAACCGCTGAGTGGAGGTGGCTGGGGGTCTAGCCCCCTCCCCCGCCGCA	1836
Db	901	GCACGGCCACCAACCGCTGAGTGGAGGTGGCTGGGGGTCTAGCCCCCTCCCCCGCCGCA	960
QY	1837	GCTCCTGGAGAACATGTACAACTGACCTTCCAGTGGCGGGCTGCCGCTGCGGTTCGA	1896
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QY	1897	CAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT	1956
Db	1021	CAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT	1080
QY	1957	GCCCAGGCTCCACGACGTGGGAGGTTCAACGGCAGCTTCAGGACAGAGCGCCTGAAGAT	2016

Db 1081 GCCCAGGCTCCACGAGCTGGGAGGTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGAT 1140
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Db 1561 ACCTTTTGTGGCCAGGATGAGTGTCCCGGAGCGGAGCAGACACGCTGCTTCCCGCGCAGG 1620
QY 2497 TCTCGGTTCTTGGCATGGGGCGAGCCGGCTGTGCTGTGCTGCTCCTGCTGTGAGCCTG 2556
Db 1621 TCTCGGTTCTTGGCATGGGGCGAGCCGGCTGTGCTGTGCTGCTCCTGCTGTGAGCCTG 1680
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Db 1741 GTTCAGGCTCGGGGGGCCCCCTGGCCTGCTTTGGCCTGCTGTGCTGGCCTGGCCTGCTGC 1800
QY 2677 CTACAGCTCCTCCTGTTCCCTGGCCAGCCAGCCCTGCCGATGCCCTGGCCAGAGCCG 2736
Db 1801 CTACAGCTCCTCCTGTTCCCTGGCCAGCCAGCCCTGCCGATGCCCTGGCCAGAGCCG 1860
QY 2737 TTGTCCCACTCCCGCTCACGGCTGCTGAGCAGCAGCAGCTTCTCTGCGAGGCGGCGAGATC 2796
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QY 2797 TTCTGGAGTCAGAACTGCCTCTGAGCTGGGCGAGACCGGCTGAGTGGCTGCTGCGGGG 2856
Db 1921 TTCTGGAGTCAGAACTGCCTCTGAGCTGGGCGAGACCGGCTGAGTGGCTGCTGCGGGG 1980
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Db 1981 CCCTGGGCTGGTGGTGTGCTGTGGCCATGCTGGTGGAGGTGCACTGTGCACTGG 2040
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QY 2977 CTGGTGCACTGCCGACACGCTCCTGGGTGAGCTTCCGCTAGCGCACGCGCCACCAATGCC 3036
Db 2101 CTGGTGCACTGCCGACACGCTCCTGGGTGAGCTTCCGCTAGCGCACGCGCCACCAATGCC 2160
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QY 3217 CTGCTCTGTCTCCTGGCATCCTGGCTGCCCTTCCACCTGCCAGGTGTTACCTGCTCATG 3276
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RESULT 15

US-10-035-045-2
; Sequence 2, Application US/10035045
; Publication No. US20030054448A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035,045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-045-2

Query Match 75.4%; Score 2687; DB 14; Length 2687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 937 GCAGGTACGTACGGTGTGATGAGTGTGAGCGCCCGGAGACCTTCCCTCCTT 996
Db 61 GCAGGTACGTACGGTGTGATGAGTGTGAGCGCCCGGAGACCTTCCCTCCTT 120
QY 997 CTTCCGACCCGTGCCAGCGACCGCTGTGAGCTGACGGCCCGCGGAGCTGCTGCAGGA 1056

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Db 841 CTGGCAGGTGAGCCCGGAGATGGGGTGTGTCTCTCTGATGTGCTCAGGCTGCCCGCAGG 900
QY 1777 GCACGGCCACACCGCTGAGCTGGAGTGGCTGGCGGCTCAGCCCGTCCCCCGCCGCA 1836
Db 901 GCACGGCCACACCGCTGAGCTGGAGTGGCTGGCGGCTCAGCCCGTCCCCCGCCGCA 960
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QY 1897 CAGCAGCGGAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT 1956
Db 1021 CAGCAGCGGAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT 1080
QY 1957 GCCCAGGCTCCACGACGTTGGGAGGTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGAT 2016
Db 1081 GCCCAGGCTCCACGACGTTGGGAGGTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGAT 1140
QY 2017 CCGTGGCACAGCTCTGAACAACAGGTGAGGTGAGGTGGGTGTCAGGCGCTGCCCGTG 2076
Db 1141 CCGTGGCACAGCTCTGAACAACAGGTGAGGTGAGGTGGGTGTCAGGCGCTGCCCGTG 1200
QY 2077 GTAGCCCCCGGCGAGGGCGCAGCCTGGGGTGGGGCCCGTTCCAGTCTCCCGTGGGCAT 2136

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QY 2197 CCGCAGTGCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCACCTCCTGCTGCTACGAC 2256
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Db 1621 TCTCGGTTCTTGGCATGGGCGAGCCGGCTGTGTGCTGCTGCTCCTGCTGCTGAGCCTG 1680
QY 2557 GCGTGGGCCCTTGTGCTGGTGTCTTGGGGCTGTTCCTGTTCAACCATCGGGACAGCCCACTG 2616
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Qy	3277	CGGCAGCCAGGGCTCAACACCCCGAGTTCTTCTGGGAGGGGGCCCTGGGGATGCCCAA	3336
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Qy	3457	TCGCTACAGAGACCTCCCGCTCTAGGTTCTGACCCCAAGTTGTTCTCCTGACCCCTGACCC	3516
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Job time : 1180 secs

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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:46:09 ; Search time 39 Seconds
(without alignments)
1426.687 Million cell updates/sec

Title: US-10-035-045-21
Perfect score: 4443
Sequence: 1 MGPRAKTIICSLFLLMWLAEL.....ERNTPAYFNMIQGYTMRD 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3231	72.7	843	3	US-09-361-631-1
3	3179	71.6	843	3	US-09-361-631-2
4	1092.5	24.6	1059	3	US-09-134-513-2
5	1089	24.5	1027	3	US-09-162-021B-2
6	1089	24.5	1027	4	US-10-268-051-8
7	1079.5	24.3	1078	1	US-08-485-588-7
8	1079.5	24.3	1078	1	US-08-484-565-7
9	1079.5	24.3	1078	2	US-08-480-751-7
10	1079.5	24.3	1078	2	US-08-943-986-7
11	1079.5	24.3	1078	3	US-08-353-784-7
12	1079.5	24.3	1078	3	US-08-484-719B-7
13	1079.5	24.3	1078	3	US-08-484-159-7
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16	1075	24.2	1079	2	US-08-480-751-8
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18	1075	24.2	1079	3	US-08-353-784-8
19	1075	24.2	1079	3	US-08-484-719B-8
20	1075	24.2	1079	3	US-08-484-159-8
21	1075	24.2	1085	1	US-08-485-588-5
22	1075	24.2	1085	1	US-08-484-565-5
23	1075	24.2	1085	2	US-08-480-751-5
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25	1075	24.2	1085	3	US-08-353-784-5
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27	1075	24.2	1085	3	US-08-484-159-5

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31	1064.5	24.0	1088	2	US-08-943-986-6	Sequence 6, Appli
32	1064.5	24.0	1088	3	US-08-353-784-6	Sequence 6, Appli
33	1064.5	24.0	1088	3	US-08-484-719B-6	Sequence 6, Appli
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36	994.5	22.4	1219	2	US-08-687-289A-6	Sequence 6, Appli
37	994.5	22.4	1219	4	US-09-435-897-6	Sequence 6, Appli
38	961.5	21.6	975	4	US-09-695-481-4	Sequence 4, Appli
39	915	20.6	863	4	US-09-619-353-14	Sequence 14, Appli
40	869	19.6	851	4	US-09-619-353-12	Sequence 12, Appli
41	857.5	19.3	854	4	US-09-619-353-10	Sequence 10, Appli
42	851.5	19.2	856	4	US-09-619-353-8	Sequence 8, Appli
43	850	19.1	835	4	US-09-619-353-7	Sequence 7, Appli
44	730	16.4	915	1	US-08-453-862-2	Sequence 2, Appli
45	730	16.4	915	2	US-08-452-734A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-361-631-7
; Sequence 7, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-0887200S
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino acid sequence
US-09-361-631-7

Query Match	78.0%;	Score	3463.5;	DB	3;	Length	669;
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						Gaps	3;
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QY	222	LLGERVARRDICIATFQETL	PTLPNQNMTESEERQRLVTI	VDKLQOSTARVVVVFSPDLTL	281		
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QY	282	YHFFNEVLQRNFTGAVWIAS	ESWAIDPVLNLTTELGHGLG	TFLGITIQSVPIPGFSEFREW	341		
Db	121	YHFFNEVLQRNFTGAVWIAS	ESWAIDPVLNLTTELGHGLG	TFLGITIQSVPIPGFSEFREW	180		
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QY	402	LLGCDKSTCTKRVVYPWQ	LLLEIKVNFLLDHI	FFDPQDQGVALLHLEIVQW	DRSQNP	461	

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QY 462 FQSVASYPLQRLKNIQDISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 521
Db 301 FQSVASYPLQRLKNIK-TSLHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 359
QY 522 PGTFNLNTEDEYECQACPNNEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTL 581
Db 360 PGTFNLNTE-----CPNNEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTL 412
QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLTLLVAYMVVVPVPPKYSTCLCRQALFPLCF 641
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QY 642 TICISCIASVRSFQIVCAFKMASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLATG 701
Db 473 TICISCIASVRSFQIVCAFKMASRFPRAYSYVWRYQGPVYSMAFITVLKMWIVVIGMLARP 532
QY 702 LSPTTRTDDPKITIVSCNPNYRNSLLFNTSLDLLLLSVVGFSPAYMGKELPTNNEAKF 761
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RESULT 2
US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-09-361-631-1
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Best Local Similarity 70.8%; Pred. No. 5.7e-303;
Matches 596; Conservative 109; Mismatches 133; Indels 4; Gaps 2;
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QY 118 EDNLLPIQEDYSNYSRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKRVRF 177
Db 121 DDDLLPILKDYSQMPHVAVIGPDNSESATVSNILSHFLIPQITYSAISDKLRKHF 180
QY 178 PALLRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVAR-RDICIAP 236
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QY 237 QETLPTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTYHFFNEVLNQFTGA 296
Db 241 QEVLPPESSQVMRSEQRQLDNILDKLRRTSARVVVVFSPPELSYFFHEVLRWNFTGF 300
QY 297 VWIASESWAIDPVHLNLTGLHGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRQS 356
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QY 357 YTCNOECDNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVVY 416
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QY 837 RR 838
Db 841 RK 842

RESULT 3
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; Sequence 2, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0

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Db	465	HLNFTSNMGEQVDFEFGDLVGNYSIINWHLSPEDGSVVFEVGHYNNVYAKKGERLFINE	524
QY	479	QDISWHTVNNTIPMSMCKRCQSGQKKPV-GIHVCCPECIDCLPGTFLNHTDEYECQA	537
Db	525	NKILWSGFSKEVPFNSCRDCLPGTRKGIIEGEPTCCPECVDCPDGEYSDET-DASACDK	583
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Db	584	CPEDYWSNENHTSCIPKQIEFLSWTEPPFGIALTLFAVLGIFLTSFVLGVFTKFRNTPIVK	643
QY	598	SAGGPMCFMLMTLLLVAYMVVYVGPVKVSTCLCRQALPPLCFTICISCIAVRSFQIVC	657
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QY	717	IVSCNPNYRNSLLFNTSLDILLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSL	776
Db	761	FITCHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS-	819
QY	777	CTFMSAYSGVLVTIVDLLVTVLNLLAISLG-----YFGPKCYMILFYPERNT	823
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; Sequence 2, Application US/09162021B			
; Patent No. 6337391			
; GENERAL INFORMATION:			
; APPLICANT: H. William Harris			
; APPLICANT: Edward M. Brown			
; APPLICANT: Steven C. Hebert			
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic			
; TITLE OF INVENTION: Species and Methods of Use Thereof			
; FILE REFERENCE: 2856.1001-007			
; CURRENT APPLICATION NUMBER: US/09/162,021B			
; CURRENT FILING DATE: 1998-09-28			
; PRIOR APPLICATION NUMBER: PCT/US97/05031			
; PRIOR FILING DATE: 1997-03-27			
; PRIOR APPLICATION NUMBER: 08/622,738			
; PRIOR FILING DATE: 1996-03-27			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 1027			
; TYPE: PRT			
; ORGANISM: squalus acanthias			
US-09-162-021B-2			
Query Match 24.5%; Score 1089; DB 3; Length 1027;			
Best Local Similarity 31.1%; Pred. No. 1e-95;			
Matches 278; Conservative 161; Mismatches 360; Indels 96; Gaps 26;			
QY	5	AKTICSLFLLWVLAPPAENSDFYLP-----GDYLLGGLFSLHANM--KGIVHLNLFQ	55
Db	2	AQLHCQLLFLGFTLLQ--SYNVSGYGNQRAQKKGDIILGGLFPIHFGVAAKQDQLKSRPE	60
QY	56	VPMCKEYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYF	114
Db	118	ATKCIRYNFR--GFRWLQAMIFAIEEINNMTLPNITLGYRIFDTCNTVSKALEATLSF	118
QY	115	LA-HEDNLLPIQE--DYSNYISRVVAVIGPDNSBSVMTVANFLSLFLPQIITYSAISDEL	171
Db	119	VAQNKIDSLNLDFCNCSHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLL	178
QY	172	RDKVRFPALLRTTPSADHHVEAMVQLMLHFRWNWIVLVSSDTYGRDNGQLLGERVARRD	231
Db	179	SNKNEYKAFRLRTIPNDEQQATAMAEIIEHFQMNWVGTLAADDYGRPGIDKFREEAVKRD	238
QY	232	ICIAFQETLPTLPQNQNMTSEERQRLVTIVDKLQOSTARVVVVVFSPLDLYHFFNEVLRLQ	291
Db	239	ICIDFSEMI-----SQYIT---QKLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRR	290
QY	292	NFTGAVWIASESWAIDPVLHNLTELHGLGTFLGITIQSVPIPGFSEFRE-----	340
Db	291	NITDRWLASEAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGFNKFLKEVHPSRSSDNG	350
QY	341	-----W-----GPOA-GPPPLSRTSQSYTCNQECNCLNAT	370
Db	351	FVKFWEETFCYFTEKTLTLQKNKVPKSHGPAAGQDGSKAGNSRRTALRHPCTGEENIT	410
QY	371	LSFNTILRLSGERVVSVYSAVVAHALHSLGCDKST-----CTK-RVVYPWQJLLE	422
Db	411	SVETPYLDYTHLRISYNNVYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVLN	470
QY	423	EIWKVNFT-LLDHQIFFDPQGDVALHLEIVQWQDRSQNP--FQSVASY-----YPLQRL	475
Db	471	HLLHLKFTNSMGEQVDFDDQDLKGNYYTIINQWLSAEDSVLFHEVGNYNAYAKPSDRLN	530
QY	476	KNIQDISWHTVNNTIPMSMCKRCQSGQKKPV-GIHVCCPECIDCLPGTFLNHTDEYE	534
Db	531	INEKKILWSGFSKVPFNSCRDCLPGTRKGIIEGEPTCCPECMACAEF-SDENDASA	589
QY	535	COACPNNWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTP	594
Db	590	CTKCPNDFWSNENHTSCIAKEIEYLSWTEPPFGIALTIFAVLGILITSFVLGVFIKFRNT	649
QY	595	IVRSAGGPMCFMLMTLLLVAYMVVYVGPVKVSTCLCRQALPPLCFTICISCIAVRSFQ	654
Db	650	IVKATNRELSYLLLSLCCFSSSLLIFIGEPRDWTCLRQPAFGISFVLCISCLVKTNR	709
QY	655	IVCAFPMASRFPRA-YSYVWRYQGPYVSMAFITVLKMVIVVIGMLATGLSPTRTDPDDP	713
Db	710	VLLVFE--AKIPTSLHRKWWGLNLQFL-LVFLCILVQIVTCTIWLVTAPSSYRNHELED	766
QY	714	KITIVSCNPNYRNSLLFNTSLDILLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSS	773
Db	767	EVIFITCDEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVW	826
QY	774	VS-LCTFMSAYSGVLVTIVDLLVTVLNLLAISLGYFG----PKCYMILFYPERNT	823
Db	827	ISFIPAVVSTY-KGFVSAVE----VIAILASSFGLLGCIYFNKCYIILFKPCRNT	876
RESULT 6			
US-10-268-051-8			
; Sequence 8, Application US/10268051			
; Patent No. 6748900			
; GENERAL INFORMATION:			
; APPLICANT: Harris, H. William			
; APPLICANT: Jury, Steven			
; APPLICANT: Russell, David R.			
; APPLICANT: Nearing, Jacqueline A			
; APPLICANT: Betka, Marlies			
; APPLICANT: Linley, Timothy			
; APPLICANT: Brown, Edward M			
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant			
; FILE REFERENCE: 2213.2004-001			
; CURRENT APPLICATION NUMBER: US/10/268,051			
; CURRENT FILING DATE: 2003-01-24			
; PRIOR APPLICATION NUMBER: 60/328,464			
; PRIOR FILING DATE: 2001-10-11			

Db 8 WVLALTHTSAYGPDQRAQKKGDIILGGLFPIHF---GVAAKD--QDLKSRPESVEICIR 62

QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121

Db 63 YNFRGRWLQAMIFAIEEINSSPALLPNTLTGYRIFDTCNTVSKALEATLSFVAQNKIDS 122

QY 122 LPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFP 179

Db 123 LNLDFCNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSRLLSNKNQFKS 182

QY 180 LIRTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICIARFQET 239

Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFEAEERDIDFSEL 242

QY 240 LPTLPQNQNTSEERQRLVTIVDKLQOQSTARVVVVVFPDPLTLYHFFNEVLRQNTGAVWI 299

Db 243 I-----SQSDEEEIQHVVEVI---QNSTAKVIVVFSGPDLEPLIKEIVRRNITGKIWL 294

QY 300 ASESWAIDPVLHNLTELHGLTFLGITIQSVPIPGFSEF-----REWGPO 344

Db 295 ASEAWASSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKXVHPRKSVHNGFAKEFWEE 354

QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382

Db 355 TFNCHLQEGAKGLPVDVTFLRGH--EESGDRFSNSSTAFRPL--CTGDENISSVETPYID 410

QY 383 ----RVVYSVYSAYAVAHALHSILGC-----DKSTCTKRVVYPWQLLEEIKVNFT 430

Db 411 YTHLRISYNVYLAIVSIAHALQDIYTCPLPGRGLFTNGSCADIKKVAEWQVLKHLRLNFT 470

QY 431 -LLDHQIFEDPDQGDVALHLEIVQWQDRSQNP--FQSVASYVPL-----QRLKNIQDIS 482

Db 471 NNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIIVKEV-GYNNVYAKKGERLFINKEKIL 529

QY 483 WHTVNTIPMSMCKRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTEDYECCQACNN 541

Db 530 WSGFSREVFFNSCRDCLAGTRKGIIEGPTCCFCEVCEPDGEYSDET-DASACNKPDD 588

QY 542 EWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGG 601

Db 589 FWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLVGFVKFRNTPIVKATNR 648

QY 602 PMCFLMLTLLVAYMVVVPVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPDPKITVS 719

Db 709 KIPTSFRK--WWGLNLQFLVFLCTFMQIVICVI-WLYTAPPSSYRNQLEDEIIFIT 764

QY 720 CNPNYRNSLLFNTSLDLLSVGVFSFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTF 779

Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---F 821

QY 780 MSAYSGVLVTIVDLLVTVLNLLAISLG----YFGPKCYMILFYPERNT 823

Db 822 IPAYASTYCKEVS-AVEVIAILAAASFGLLACIFFNKIYIILFKPSRNT 868

RESULT 8

US-08-484-565-7

Sequence 7, Application US/08484565

Patent No. 5763569

GENERAL INFORMATION:

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

TITLE OF INVENTION: MOLECULES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,565

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 213/006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1078 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-484-565-7

Query Match 24.3%; Score 1079.5; DB 1; Length 1078;

Best Local Similarity 31.4%; Pred. No. 9.1e-95;

Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPAENSDFYLP-----GDYLLGGLFSLHANMKGIVHLNFLQVPMCKEYEVKVG 68

Db 8 WVLALTHTSAYGPDQRAQKKGDIILGGLFPIHF---GVAAKD--QDLKSRPESVEICIR 62

QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121

Db 63 YNFRGRWLQAMIFAIEEINSSPALLPNTLTGYRIFDTCNTVSKALEATLSFVAQNKIDS 122

QY 122 LPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFP 179

Db 123 LNLDFCNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSRLLSNKNQFKS 182

QY 180 LIRTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICIARFQET 239

Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFEAEERDIDFSEL 242

QY 240 LPTLPQNQNTSEERQRLVTIVDKLQOQSTARVVVVVFPDPLTLYHFFNEVLRQNTGAVWI 299

Db 243 I-----SQYDEEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWL 294
QY 300 ASESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGFSEF-----REWGPO 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGREFLKXVHPRKSVHNGFAKEFWEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLOEGAKGPLPVDITFLRGH--EESGDRFSNSSTAFLRPL--CTGDENISSVETPYID 410
QY 383 -----RVVYSVYSAVYAVAHALHSLGCG-----DKSTCTKRVVYPWQLLEEIKVNF 430
Db 411 YTHLRISYNVYLAIVYIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFT 470
QY 431 -LLDHQIFPDQGDVALHLEIVQWQWDRSQNP--FQSVASYYP-----QRQLKNIQDIS 482
Db 471 NNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIIVKEV--GYNVYAKKGERLFINEEKIL 529
QY 483 WHTVNTIPMSCKRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTEDYEYEQACPN 541
Db 530 WSGFSREVFPNSCRDCLAGTRKGIIEGPTCCFECVCPDGEYSDET-DASACNKCDD 588
QY 542 EWSYQSETSCFKRLQVLEWHEAPTIAVALLAALGLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKIEFLSWTEPFGIALTLFAVLGIELTAFVLGVFIKFRNTPIVKATNR 648
QY 602 PMCFMLTLTLVAYMVVYVVPVPPKVVSTCLCRQALFPLCFTICISCIATVRSQIVCAF-- 659
Db 649 ELSYLLLFLLCCFSSSLFFIGEPQDWTCLRPAPAGISFVLCISILVKTNRVLLVFEA 708
QY 660 KMASRFPRAYSVWRYQGPVSMAPITVLKMWIVVIGMLATGLSPTRTDDPKITIVS 719
Db 709 KIPTSFHRK---WGLNLQFLLVFLCTFMQIVICVI-WLYTAPPSSYRNQBLEDEIIFIT 764
QY 720 CNPNYRNSLFTNSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFTTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFIVWIS---F 821
QY 780 MSAYSGVLVTIIVLLVTLNLLAISLG----YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYCKFVS-AVEVIAILAAAFGLLACIFFNFKIYIILFKPSRNT 868

RESULT 9
US-08-480-751-7
; Sequence 7, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751

; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-751-7

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPAENSDPYLP-----GDYLLGLFSLHANKMGIVHLNLFQVEMCKEYEVKVG 68
Db 8 WVLALTWHTSAYGPDQRAQKKGDIILGLFPIHF---GVAAKD--QDLKSRPESVECIR 62
QY 69 YNL-----MQAMRFAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFWLQAMIFAIEEINSSPALLNLTGRIYFDTCTNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNVISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKDKVFP 179
Db 123 LNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLLSNKNQFKS 182
QY 180 LLRTTPSADHHVEAMVOLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICI 239
Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFEAEERDIDFSEL 242
QY 240 LPTLPQNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLVHPFNEVLQNFTGAV 299
Db 243 I-----SQYDEEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWL 294
QY 300 ASESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGFSEF-----REWGPO 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGREFLKXVHPRKSVHNGFAKEFWEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLOEGAKGPLPVDITFLRGH--EESGDRFSNSSTAFLRPL--CTGDENISSVETPYID 410
QY 383 -----RVVYSVYSAVYAVAHALHSLGCG-----DKSTCTKRVVYPWQLLEEIKVNF 430

Db 411 YTHLRISYNNVLAIVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFT 470
QY 431 -LLDHQIFFDPQGDVALHLEIVQWQDRSNP--FQSVASYPL-----QRQKNIQDIS 482
Db 471 NMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFEKV-GYNNVYAKKGERLFINEEKIL 529
QY 483 WHTVNTIPMSCKRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTDEYECQACPN 541
Db 530 WSGFSREVFPFNSCRDCLAGTRKGIIEGEPTCCFECVCEPDGEYSDET-DASACNKCDD 588
QY 542 EWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNR 648
QY 602 PMCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAF-- 659
Db 649 ELSYLLLFLLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKNRVLVFEA 708
QY 660 KMASRFPFRAYSWRYQGPVSMFITYLVKMVIVVIGMLATGLSPTRTDDPKITIVS 719
Db 709 KIPTSFRK---WWGLNLQFLVFLCTFMQIVICVI-WLYTAPSSYRNQELDEIIFIT 764
QY 720 CNPNYRNSLLFNTSLDLLSVVGFSAFYMGKELPTNNNEAKFITLSMTFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---F 821
QY 780 MSAYSGVLVTIVDILLVTLNLAISLG---YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYCKFVS-AVEVIAILAAASFGLLACIFFENKIYIILFKPSRNT 868

RESULT 10

US-08-943-986-7
; Sequence 7, Application US/08943986
; Patent No. 5962314
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,986
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,565
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993

; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-986-7

Query Match 24.3%; Score 1079.5; DB 2; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPANSDFYLP-----GDYLLGGLFSLHANMKGIVHLNFLQVPMCKEYEVKVG 68
Db 8 WVLLALTWHTSAYGPDQRAKKGDIIILGGLFIHF---GVAAKD--QDLKSRPESVECI 62

QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFRWLQAMIFAIEEINSSPALLPNLTGLYRIFDTCTNTVSKALEATLSFVAQNKIDS 122

QY 122 LPIQE--DYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRPFA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSRLLSNKNQFKS 182

QY 180 LLRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICI AFQET 239
Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFREEAEERDICI DFSEL 242

QY 240 LPTLQPNQNMTESEORQLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLNRQFTGAVWI 299
Db 243 I-----SQYSDEEEIQHVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWL 294

QY 300 ASESWAIDPVLHNLTELGHGLTFLGITIQSVPIPGSEF-----REWGPQ 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKKVHPRKSVHNGFAKEPWEE 354

QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNLTLSGE----- 382
Db 355 TFNCHLQEGAKGPLPVDTFLRGH--EESGDRFSSNSTAFRPL--CTGDENISSVETPYID 410

QY 383 ----RVVYSVYSAVYAVAHLSLLGC-----DKSTCTKRVVYPWQLLEEIKVNFT 430
Db 411 YTHLRISYNNVLAIVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFT 470

QY 431 -LLDHQIFFDPQGDVALHLEIVQWQDRSNP--FQSVASYPL-----QRQKNIQDIS 482
Db 471 NMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFEKV-GYNNVYAKKGERLFINEEKIL 529

QY 483 WHTVNTIPMSCKRQSGQKKPV-GIHVCCFECIDCLPGTFLNHTDEYECQACPN 541
Db 530 WSGFSREVFPFNSCRDCLAGTRKGIIEGEPTCCFECVCEPDGEYSDET-DASACNKCDD 588

QY 542 EWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNR 648

QY 602 PMCFLMLTLLLVAYMVVVPVYVGPVKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAF-- 659

Db 649 ELSYLLLSLLCCFSSSLFFIGEPODWTCLRLQPAFGISFVLCISCLVTKNRVLLVFEA 708
QY 660 KMASRFPRAYSYWRVQGPVVSMAFIVLKMVIVVIGMLATGLSPTRTDPDPKITIVS 719
Db 709 KIPTSFRK---WWGLNLQFLVFLCTFMQIVICVI-WLYTAPSSSYRNQELDEIIFIT 764
QY 720 CNPNYRNSLLENTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---F 821
QY 780 MSAYSGVLVTIVDLLVTVNLNLAISLG---YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYCKFVS-AVEVIAILAAASFGLLACIFFENKIYIILFKPSRNT 868

RESULT 11

US-08-353-784-7

Sequence 7, Application US/08353784

Patent No. 6011068

GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,784

FILING DATE: 9 December, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 8

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 209/069

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-784-7
Query Match 24.3%; Score 1079.5; DB 3; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPAENSDFYLP-----GDYLLGGLFSLHANMKGIVHLNFLQVPMCKEYEVKVG 68
Db 8 WVLALALTWHTSAYGPDQRAQKKGDIILGGLFPIHF---GVAAKD--QDLKSRPESVEICR 62
QY 69 YNL-----MQAMRFAVEEINNDSSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFRWLQAMIFAEEINSSPALLPNTLGYRIFDTCNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNYISRVAVIGPDNSESVMTVANFSLFLLPQITYSAISDELDRDKVRPPA 179
Db 123 LNLDEFNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSSRLSNKNQFKS 182
QY 180 LLRTTPSADHHVEMVQLMLHFRWNWIIVLVSSDITYGRDNGQLLGERVARRDICIATQET 239
Db 183 FLRTIPNDEHQATAMADIIIEYFRWNWVGTTAAADDDYGRPGIEKFREEAEERDIDFSEL 242
QY 240 LPTLPQNQNTSEBRQLVTIVDKLQQSTARVVVVFSPDLTYLHFFNEVLQNFTGAVWI 299
Db 243 I-----SQYSDEEIQHVVEVI---QNSTAKVIVVVFSSGPDLEPLIKEIVRNITGKIWL 294
QY 300 ASESWAIDPVLHNLTELGLTGLTIGITIQSVPIPGFSEF-----REWGPO 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAQIPGREFLKKVHPKSVHNGFAKEFWE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNLTILRLSGE----- 382
Db 355 TFNCHLQEGAKGELPVDTFLRGH--EESGDRFSNSSTAFLPL--CTGDENISSVETPYID 410
QY 383 ----RVVYSVYSAYVAHAHALHSLLC-----DKSTCTKRVVYPWQLLEIWKVNFT 430
Db 411 YTHLRISYNVYLAVYSIAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQLKHLRHLNFT 470
QY 431 -LLDHQIFFDPOGDVALHLEIVQWQWDRSQNP--FQSVASYPL-----ORQLKNIQDIS 482
Db 471 NNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEV-GYYNVYAKKGERLFINEEKIL 529
QY 483 WHTVNNTIPMSCKRQCSGQKKPV-GIHVCCFECIDCLPGTFLNHTDEYECQACPNN 541
Db 530 WSGFSREVPFNSCRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDET-DASACNKCDD 588
QY 542 EWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPFPGIALTLFAVLGIFLTAFLVGLVIFKFRNTPIVKATNR 648
QY 602 PMCFLMLTLLLVAYMVVYPVVGPPKVVSTCLCRQALPPLCTTICISIAVRSFQIVCAF-- 659
Db 649 ELSYLLLSLLCCFSSSLFFIGEPODWTCLRLQPAFGISFVLCISCLVTKNRVLLVFEA 708
QY 660 KMASRFPRAYSYWRVQGPVVSMAFIVLKMVIVVIGMLATGLSPTRTDPDPKITIVS 719
Db 709 KIPTSFRK---WWGLNLQFLVFLCTFMQIVICVI-WLYTAPSSSYRNQELDEIIFIT 764
QY 720 CNPNYRNSLLENTSLDLLSVVGFSPAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---F 821
QY 780 MSAYSGVLVTIVDLLVTVNLNLAISLG---YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYCKFVS-AVEVIAILAAASFGLLACIFFENKIYIILFKPSRNT 868

RESULT 12
US-08-484-719B-7
; Sequence 7, Application US/08484719B
; Patent No. 6031003
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen,
; APPLICANT: Manuel F. Balandrin,
; APPLICANT: Forrest H. Fuller, Eric G.
; APPLICANT: Delmar, Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Word
; SOFTWARE: FastSEQ for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,719B
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Douglas C. Murdock
; REGISTRATION NUMBER: 37,549
; REFERENCE/DOCKET NUMBER: 213/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-719B-7

Query Match 24.3%; Score 1079.5; DB 3; Length 1078;
Best Local Similarity 31.4%; Pred. No. 9.1e-95;
Matches 279; Conservative 160; Mismatches 342; Indels 107; Gaps 27;

QY 16 WVLAEPANSDFYLP-----GDYLLGLGLESLSHANMKGIVHLNLFQVPMCKEYEVKVIG 68
Db 8 WVLLALTWHTSAYGPDQRAKKGDIILGGLFPIHF---GVAAKD--QDLKSRPESVECIR 62
QY 69 YNL-----MQAMRPAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA-HEDNL 121
Db 63 YNFRGFRWLQAMIPAEIEINSSPALLPNTLTGRIFDTCNTVSKALEATLSFVAQNKIDS 122
QY 122 LPIQE--DYSNYSIRVVAVIGPDNSESVMVTANFLSLFLLPQITYSAISDELDRDKVRPPA 179
Db 123 LNLDFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSNKNQFKS 182
QY 180 LLRTTPSADHHEAMVQMLHFRWNWIIIVSSDITYGRDNGQLLGERVARRDICIATFQET 239
Db 183 FLRTIPNDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFREEAEERDIDFSEL 242
QY 240 LPTLPQNQNMTEERQRLVTIVDKLQQSTARVVVVVSPDLTLYHFFNEVLNRQNETGAVWI 299
Db 243 I-----SQYSDEEIQHVVEVI---QNSTAKVIVVFSGGPDLEPLIKEIVRNITGKIWL 294
QY 300 ASESWAIDPVLHNLTELHGLGTFLGITIQSVPIPGSEF-----REWGPO 344
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKKVHPRKSVHNGFAKEFWEE 354
QY 345 A-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 355 TFNCHLQEGAKGPLPVDTFLRGH--EESGDRFSNSTAFRPL--CTGDENISSVETPYID 410
QY 383 ---RVVYSVYSVAVVAHALHSLG-----DKSTCTKRVVYPWQLLEEIKVKNFT 430
Db 411 YTHLRISYNVYLAIVYIAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQVLKHLRHLNFT 470
QY 431 -LLDHQIFFDPQGDVALHLEIVQWQDRSQNP--FQSVASYPL-----QRLKNIQDIS 482
Db 471 NMGEQVTFDECGDLVGNYSIINWHLSPEDGSIIVKEV-GYINVYAKKGERLFINEEKIL 529
QY 483 WHTVNTIPMSCKRCQSQGKKPV-GIHVCCBECIDCLPGTFLNHTEDYEYECQACPNN 541
Db 530 WSGFSREVPFNSCRDCLAGTRKGIIEGEPTCCBCEVCPDGEYSDET-DASACNKPDD 588
QY 542 EWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGLSTLAILVIFWRHFQTPIVRSAGG 601
Db 589 FWSNENHTSCIAKEIEFLSWTEPFGLTALTLFAVLGIFLTAFLVGVIKFRNTPIVKATNR 648
QY 602 PMCFLMLTLLVAYMVVVPVPPKVVSTCLCRQALPCLCFTICISCIASVRSFQIVCAF-- 659
Db 649 ELSYLLLFSLCCFSSSLFFIGEPQDWTCLRQAPAGISFVLCISCLVKTNRVLLVFEA 708
QY 660 KMASRFPRAYSYVWRYQGPVVSMAFITVLKMVIVIGMLATGLSPTTRTDPDDPKITIVS 719
Db 709 KIPTSFRK--WWGLNLQFLVFLCTFMQIVICVI-WLYTAPSSSYRNQOELEDEIFIT 764
QY 720 CNPNYRNSLLENTSLDLLSVVGFSFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTF 779
Db 765 CHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWIS---F 821
QY 780 MSAYSGVLVTIVDLLVTVLNLLAISLG----YFGPKCYMILFYPERNT 823
Db 822 IPAYASTYKFKVS-AVEVIAILAAASFGLLACIFFNKIYIILFKPSRNT 868

RESULT 13
US-08-484-159-7
; Sequence 7, Application US/08484159
; Patent No. 6313146
; GENERAL INFORMATION:
; APPLICANT: Bradford C. Van Wagenen
; APPLICANT: Manuel F. Balandrin
; APPLICANT: Eric G. Del Mar
; APPLICANT: Edward F. Nemeth
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,588
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-588-8
;
; Query Match 24.2%; Score 1075; DB 1; Length 1079;
; Best Local Similarity 31.4%; Pred. No. 2.5e-94;
; Matches 282; Conservative 166; Mismatches 327; Indels 124; Gaps 33;
;
QY 10 SLFFLLWVLAEPANSEDFYLP-----GDYLLGLFSLHANMKGIVHLNLFQVPMCKEY 62
Db 9 ALLALAW-----HSSAYGPDQRAQKGDIIILGLFPPIHF---GVAAKD--QDLKSRPE 56
QY 63 EVKVIQYNL-----MQAMRFAVEEINNDSLLPGVLGLYEIVDVC-YISNNVQPVLYFLA 116
Db 57 SVECIYRNGFRWLQAMIFAIEEINSSPSLLPNMTGLYRIFDTCNTVSKALEATLSFVA 116
QY 117 -HEDNLLPIQE--DYSNYSIRVAVAVIGPDNSESVMVTVANFLSLFLLPQITYSAISDELRD 173
Db 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSKLLSN 176
QY 174 KVRFPALLRTTPSADHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDIC 233
Db 177 KNQYKSLRTPINDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFEEREAERDIE 236
QY 234 IAFQETLPTLPQNQNMTSEERQRLVTIVDKLQOQSTARVVVVVSPDLTLYHFFNEVLRQNF 293
Db 237 IDFSLI-----SQYSEEEIQQVVEVI---QNSTAKVIVVSSGPDLEPLIKEIVVRNI 288
QY 294 TGAWVIASEWAIDPVLNLTGLCH-LGTFLGITIQSVPIPGFSEF----- 338
Db 289 TGRWLASEAWASSSLI-AMPEYFHVVGTTIGFGLKAGQIPGFREFLQKVHPKSVHNGF 347
QY 339 -REWGPQA-----GPPPLSRTSQSYTCNQECNCLNATLSFNTILRLSGE----- 382
Db 348 AKFEWBEETFNCHLQEGAKGPLVDVTFVRSH--EEGGRNLLNSSTAFRPL--CTGDENINS 403
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QY 383 -----RVVYSVYSAYAVAHLSLLGC-----DKSTCTKRVVVPWQLLEE 423
Db 404 VETPYMDYEHLEIRISYNYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKH 463
QY 424 IKVKNFT-LLDHQIFDPQGDVALHLEIVQWQWDRSQNP--FQSVASYVPL-----QRQL 475
Db 464 LRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIKFKEV-GYNNVYAKKGERLF 522
QY 476 KNIQDISWHTVNNTPMSMCKRCQSGQKKKPV-GIHVCCFECIDCLPGFNLNHTEDEYE 534
Db 523 INEEKILWSGFSREVFPSCNRDCQAGTRKGIIEGEPTCCFECVCECPDGEYSGET-DASA 581
QY 535 CQACPNNEWSYQSETSCFKRQLVFLEWHEAPTIALLAALGFLSTLAILVIFWRHFQTP 594
Db 582 CDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIFLTAFLVGLGVFIKFRNTP 641
QY 595 IVRSAGGPMCFMLTLLVAYMVVYVVGPKVSTCLCRQALFPLCFTTICISCIARVSFQ 654
Db 642 IVKATNRELSYLLLSLCCFSSSLFFIGEPQDWTCLRLQPAFGISFVLCISCLVKTNR 701
QY 655 IVCAFOMASRFFPRAY--SYW-VRYQGPYVSMARITVLMVIVVIGMLATGLSPTTRTDPD 711
Db 702 VLLVFE--AKIPTSFHRKMWGLNLQ---FLLVFLCTFMQILICIIWLVTAPSSYRNHEL 756
QY 712 DPKITIVSCNPYRNSLLFNTSL---DLLSVGVFSFAYMGKELPTNYNEAKFITLSMTF 768
Db 757 EDEIIFITC---HEGSLMALGSLIGYTCLLAAICPFFFAFKSRKLPENFNEAKFITFSMLI 813
QY 769 YFTSSVSLCTFMSAYSGLVTVIVDLLVTVLNLLAISLG---YFGPKCYMILFYPERNT 823
Db 814 FFIVWIS---FIPAYASTYKFSV-AVEVIAILAAASFGLLACIFFNKVYIILFKPSRNT 868
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RESULT 15

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US-08-484-565-8
; Sequence 8, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
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/ APPLICATION NUMBER: U.S. 08/009,389
/ FILING DATE: 23 February, 1993
/ APPLICATION NUMBER: U.S. 08/017,127
/ FILING DATE: 12 February, 1993
/ APPLICATION NUMBER: U.S. 07/934,161
/ FILING DATE: 21 August, 1992
/ APPLICATION NUMBER: U.S. 07/834,044
/ FILING DATE: 11 February, 1992
/ APPLICATION NUMBER: U.S. 07/749,451
/ FILING DATE: 23 August, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heber, Sheldon O.
/ REGISTRATION NUMBER: 38,179
/ REFERENCE/DOCKET NUMBER: 213/006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1079 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-484-565-8

Query Match 24.2%; Score 1075; DB 1; Length 1079;
Best Local Similarity 31.4%; Pred. No. 2.5e-94;
Matches 282; Conservative 166; Mismatches 327; Indels 124; Gaps 33;

QY 10 SLFFLLWVLAEPAEENSDFYLP-----GDYLLGLFSLHANMKGIIVHLNFIQVPMCKEY 62
Db 9 ALLALAW-----HSSAYGPDQRAQKKGDIILGGLFPIHF---GVAAKD--QDLKSRPE 56

QY 63 EVKVIQYNL-----MQAMRFAVEEINNDSLLPGVLLGYEIVDVC-YISNNVQPVLYFLA 116
Db 57 SVECIRYNFRGFRWLQAMIFAIEEINSSPSPLLPNTLGYRIFDTCNTVSKALEATLSFVA 116

QY 117 -HEDNLLPIQE--DYSNVIISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRD 173
Db 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLLSN 176

QY 174 KVRFPALLRTTPSADHHVEAMVOLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDIC 233
Db 177 KNOYKSFRLTIPNDEHQATAMADIIIEYFRWNWVGCTIAADDDYGRPGIEKFREEAEERDIC 236

QY 234 IAFQETLPTLPQNQNTSEERQLVTIVDKLQOSTARVWVVFSPDLTLVHFFNEVLQNF 293
Db 237 IDFSELI-----SQYSDEEIIQQVVEVI---QNSTAKVIVVFSSGPDLEPLIKEIVRNI 288

QY 294 TGAVWIASESWAIDPVLHNLTELGH-LGTFELGITIQSVPIPGFSEF----- 338
Db 289 TGRWLASEAWASSSLI-AMPEYFHVVGTTIGFLKAGQIPGREFLOKVHPRKSVHNGF 347

QY 339 -REWGPOA-----GPPPLSRTSQSYTCNQECDNCLNATLSFNTILRLSGE----- 382
Db 348 AKEFWEETFNCHLOEGAKGPLPVDTFVRSH--BEGGNRLNLSSTAERPL--CTGDENINS 403

QY 383 -----RVVYSVYSAYAVAHALHSLGC-----DKSTCKRVVYPWQLLEE 423
Db 404 VETPYMDYEHRLRISYNYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKH 463

QY 424 IWKVNFT-LLDHOIFEDPDQDVALHLEIVQWQWDRSQNP--FQSVASYPL-----QRQL 475
Db 464 LRHLNFTNNMGEQVTFDECGDLVGNYSIINHLSPEDGSI VFKEV-GYNNVYAKKGERLF 522

QY 476 KNIQDISWHTVNNTIIPMSCKSKRCQSGQKKPV-GIHVCCFECIDCLPGTFNLHTEDEYE 534
Db 523 INEEKILWSGFSREVPFNSCSRDCQAGTRKGIIEGPTCCFECVECPDGEYSGET-DASA 581

QY 535 CQACPNNEWSYQSETSCFKRQLVFLWEHEAPTIAVALLAALGFLSTLAILVFWRHFTPT 594
Db 582 CDKCPDDFWSNENTHTSCIAKEIEFLAWTEPFGIALTLFAVLGIFLTAFLVGLGVFIKFRNTP 641

QY 595 IVRSAGGPMCFMLMTLLLVAYMVVVPVVGPPKVSTCLCRQALFPLCFTTICISCIAVRSFQ 654
Db 642 IVKATNRELSYLLLFSLCCFSSSLFFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNR 701
QY 655 IVCAFKMASRFRPRAY--SYW-VRYQGPYVSNMAFITVLKMVIVVIGMLATGLSPTRTDPD 711
Db 702 VLLVFE--AKIPTSFHRKWWGLNLQ---FLLVFLCTFMQILICIIWLVTAPPSSYRNHEL 756
QY 712 DPKITIVSCNPVNRNSLLFNTSL---DLLLSVVGFSPAYMGKELPTNYNEAKFITLSMTF 768
Db 757 EDEIIIFITC---HEGSLMALGSLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLI 813
QY 769 YFTSSVSLCTFMSAYSGVLVTIVDLLVTVLNLLAISLG----YFGPKCYMILFYPERNT 823
Db 814 FFIVWIS---FIPAYASTYGFVS-AVEVITAILAASFGLLACIFFENKVYIILFKPSRNT 868

Search completed: November 30, 2004, 13:56:29
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 13:54:59 ; Search time 150 Seconds
(without alignments)
1983.926 Million cell updates/sec

Title: US-10-035-045-21
Perfect score: 4443
Sequence: 1 MGPRAKTICSLFLLWVLAEE.....ERNTPAYFNSMIQYTMRRD 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4443	100.0	839	14	US-10-035-045-21
3	4443	100.0	839	14	US-10-179-373-6
4	4443	100.0	839	16	US-10-725-103-6
5	4443	100.0	839	16	US-10-725-489-6
6	4443	100.0	839	16	US-10-725-080A-6
7	4443	100.0	839	17	US-10-725-472A-6
8	4443	100.0	839	17	US-10-725-276-21
9	4443	100.0	839	17	US-10-770-127-198
10	4422	99.5	839	14	US-10-246-785-4
11	4392.5	98.9	838	10	US-09-927-315-9
12	4392.5	98.9	838	14	US-10-190-417-9
13	3463.5	78.0	669	13	US-10-124-598-7

14	3463.5	78.0	669	14	US-10-096-144-7	Sequence 7, Appli
15	3463.5	78.0	669	14	US-10-225-567A-683	Sequence 683, App
16	3231	72.7	843	10	US-09-927-315-7	Sequence 7, Appli
17	3231	72.7	843	13	US-10-124-598-1	Sequence 1, Appli
18	3231	72.7	843	14	US-10-096-144-1	Sequence 1, Appli
19	3231	72.7	843	14	US-10-246-785-6	Sequence 6, Appli
20	3231	72.7	843	14	US-10-190-417-7	Sequence 7, Appli
21	3231	72.7	843	14	US-10-179-373-17	Sequence 17, Appl
22	3231	72.7	843	15	US-10-436-715-38	Sequence 38, Appl
23	3231	72.7	843	15	US-10-436-715-70	Sequence 70, Appl
24	3231	72.7	843	16	US-10-725-103-17	Sequence 17, Appl
25	3231	72.7	843	16	US-10-725-489-17	Sequence 17, Appl
26	3231	72.7	843	16	US-10-725-080A-17	Sequence 17, Appl
27	3231	72.7	843	17	US-10-725-472A-17	Sequence 17, Appl
28	3179	71.6	843	10	US-09-927-315-8	Sequence 8, Appli
29	3179	71.6	843	13	US-10-124-598-2	Sequence 2, Appli
30	3179	71.6	843	14	US-10-096-144-2	Sequence 2, Appli
31	3179	71.6	843	14	US-10-190-417-8	Sequence 8, Appli
32	2532.5	57.0	661	14	US-10-246-785-5	Sequence 5, Appli
33	1456.5	32.8	840	10	US-09-361-652-1	Sequence 1, Appli
34	1456.5	32.8	840	10	US-09-927-315-1	Sequence 1, Appli
35	1456.5	32.8	840	14	US-10-246-785-3	Sequence 3, Appli
36	1456.5	32.8	840	14	US-10-190-417-1	Sequence 1, Appli
37	1456.5	32.8	840	14	US-10-159-339-12	Sequence 12, Appl
38	1456.5	32.8	840	14	US-10-179-373-16	Sequence 16, Appl
39	1456.5	32.8	840	15	US-10-436-715-39	Sequence 39, Appl
40	1456.5	32.8	840	15	US-10-436-715-69	Sequence 69, Appl
41	1456.5	32.8	840	16	US-10-725-103-16	Sequence 16, Appl
42	1456.5	32.8	840	16	US-10-725-489-16	Sequence 16, Appl
43	1456.5	32.8	840	16	US-10-725-080A-16	Sequence 16, Appl
44	1456.5	32.8	840	17	US-10-725-472A-16	Sequence 16, Appl
45	1446.5	32.6	842	15	US-10-436-715-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-897-427A-4
; Sequence 4, Application US/09897427A
; Patent No. US20020160424A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEWSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-4

Query Match	100.0%;	Score 4443;	DB 9;	Length 839;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 839;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MGPRAKTICSLFLLWVLAEPNDSFYLPDYLGLGFLSHANMKGIVHNLFLQVPMCK	60	
Qy	61	EYEVKVGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCIYISNNVQPVLYFLAHEDN	120	
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Qy	121	LLPTQEDYSNYSRVVAVIGPDNSESVMTVANFLSLFLPQITYSAISDELDRKVRFPAL	180	

Db 121 LLPIQEDYSNYSRVAVIGPDNSESVMTVANFSLFLLPQITYSAISDELDRKVRFPAL 180
QY 181 LRTTPSADHHVEAMVQMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRDICIATFQETL 240
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QY 241 PTLQPNQNTSEERQRLVTIIVDKLQOSTARVVVVFSPDLTLYHFFNEVLQNTGAVWIA 300
Db 241 PTLQPNQNTSEERQRLVTIIVDKLQOSTARVVVVFSPDLTLYHFFNEVLQNTGAVWIA 300
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Db 301 SESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGSEFREWGPQAGPPPLSRTSQSYTCN 360
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Db 361 QECNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVPVWPWL 420
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Db 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
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RESULT 2

US-10-035-045-21
; Sequence 21, Application US/10035045
; Publication No. US20030054448A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: TLR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035,045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-045-21

Query Match 100.0%; Score 4443; DB 14; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 EYEVKVIQYNLMQAMRFAVEEINNDSLLPGVLLGYEIVDVCIYISNNVQPVLYFLAHEDN 120
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Db 121 LLPIQEDYSNYSRVAVIGPDNSESVMTVANFSLFLLPQITYSAISDELDRKVRFPAL 180
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Db 301 SESWAIDPVLHNLTELGHGTLGTLGITIQSVPIPGSEFREWGPQAGPPPLSRTSQSYTCN 360
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Db 361 QECNCLNATLSFNTILRLSGERVVYSVAVYVAHALHSLGCDKSTCTKRVPVWPWL 420
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Db 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
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RESULT 3

US-10-179-373-6
; Sequence 6, Application US/10179373
; Publication No. US20030232407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG

APPLICANT: ECHEVERRI, FERNANDO
TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
FILE REFERENCE: 078003-0291566
CURRENT APPLICATION NUMBER: US/10/179,373
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/300,434
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/304,749
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/310,493
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/331,771
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/339,472
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/372,090
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/374,143
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 6
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
US-10-179-373-6

Query Match 100.0%; Score 4443; DB 14; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 SESWAIDPVLHNLTELGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
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421 LEEIWKVNFLLDHIQIFDPPQGDVALHLEIVQWQDRSQNPFQSVASYYPQLRQLKNIQD 480
421 LEEIWKVNFLLDHIQIFDPPQGDVALHLEIVQWQDRSQNPFQSVASYYPQLRQLKNIQD 480
481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
481 ISWHTVNTIPMSMCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600

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Db 601 GPMCFLMLTLLLVAYMVVPPVKVSTCLCROALFPLCFTICISCIASVRSFQIVCAFK 660
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Db 661 MASRFPRAYSYWRVYQGPVVSMAFITVLKMWIVVIGMLATGLSPTRTDDPKITIVSC 720
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Db 781 SAYSGVLVTIVDILLVTLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 839

RESULT 4

US-10-725-103-6
Sequence 6, Application US/10725103
Publication No. US20040175792A1
GENERAL INFORMATION:
APPLICANT: ZOLLER, MARK
APPLICANT: LI, XIAODONG
APPLICANT: STASZEWSKI, LENA
APPLICANT: O'CONNELL, SHAWN
APPLICANT: ZOZULYA, SERGEY
APPLICANT: ADLER, JON
APPLICANT: XU, HONG
APPLICANT: ECHEVERRI, FERNANDO
TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
FILE REFERENCE: 078003-0291566
CURRENT APPLICATION NUMBER: US/10/725,103
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/300,434
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/304,749
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/310,493
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/331,771
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/339,472
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/372,090
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/374,143
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 6
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
US-10-725-103-6

Query Match 100.0%; Score 4443; DB 16; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLVPMCK 60
1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGLGGLFSLHANMKGIVHLNQLVPMCK 60
61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCIYISNNVQVLYFLAHEDN 120
61 EYEVKVIYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCIYISNNVQVLYFLAHEDN 120
121 LLPIQEDYSNYSRVRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
121 LLPIQEDYSNYSRVRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180

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Db	181	LRTTPSADHHVEAMVQLMLHFRWNWII	VLVSSD	TYGRDNGQLLGERVARRD	CIAFOETL	240	
QY	241	PTLQPNQNM	TSEERQRLVTI	VDKLQOSTARVVVVFSPDL	TLTYHFFNEVL	RQNTGAVWIA 300	
Db	241	PTLQPNQNM	TSEERQRLVTI	VDKLQOSTARVVVVFSPDL	TLTYHFFNEVL	RQNTGAVWIA 300	
QY	301	SESWAIDPVLHNL	TELGHGTFLGITIQSVPI	PGFSEFREWGPQAGPPPL	SRTSQSYTCN	360	
Db	301	SESWAIDPVLHNL	TELGHGTFLGITIQSVPI	PGFSEFREWGPQAGPPPL	SRTSQSYTCN	360	
QY	361	QECNCLNATLS	FNITLRLSGERVVYS	SAVYAVAHALHSLGCDKSTCT	KRVVYPWQL	420	
Db	361	QECNCLNATLS	FNITLRLSGERVVYS	SAVYAVAHALHSLGCDKSTCT	KRVVYPWQL	420	
QY	421	LEEIWKVNFTLL	DHQIFFDPQGDVALHLEIVQWQDR	SQNPFSVASYPL	QRQLKNIQD	480	
Db	421	LEEIWKVNFTLL	DHQIFFDPQGDVALHLEIVQWQDR	SQNPFSVASYPL	QRQLKNIQD	480	
QY	481	ISWHTVNNTI	PMSMCKRCQSGQKKKPVGTHVCC	FECDLPGTFLNHTDEYECQ	ACP	N 540	
Db	481	ISWHTVNNTI	PMSMCKRCQSGQKKKPVGTHVCC	FECDLPGTFLNHTDEYECQ	ACP	N 540	
QY	541	NEWSYQSETSC	FKRQLVFLEWHEAPTIAVALLAAL	GFLSTLAILVIFWRHQTPI	VR	SAG 600	
Db	541	NEWSYQSETSC	FKRQLVFLEWHEAPTIAVALLAAL	GFLSTLAILVIFWRHQTPI	VR	SAG 600	
QY	601	GP	MFLMTLLL	VAYMVVPVYVGP	KVSTCLCRQALFPLCFTICIS	CIASVRSFQIVCAF	N 660
Db	601	GP	MFLMTLLL	VAYMVVPVYVGP	KVSTCLCRQALFPLCFTICIS	CIASVRSFQIVCAF	N 660
QY	661	MASRFP	PRAYS	YWVRYQGPV	SMAFITVLKMVI	VIGMLATGLSP	TRTDEDDPKITIVSC 720
Db	661	MASRFP	PRAYS	YWVRYQGPV	SMAFITVLKMVI	VIGMLATGLSP	TRTDEDDPKITIVSC 720
QY	721	NP	NYRNSLL	FN	TS	LDLLSVVGFSFAYMGKELPTNYNEAK	FITLSMTFYFTSSVSLCTFM 780
Db	721	NP	NYRNSLL	FN	TS	LDLLSVVGFSFAYMGKELPTNYNEAK	FITLSMTFYFTSSVSLCTFM 780
QY	781	SAYS	GV	LVTIVD	LLVTVLNLLAISLGYFGPKCYMILFYPERNT	PAYFNSMIQYTM	RDRD 839
Db	781	SAYS	GV	LVTIVD	LLVTVLNLLAISLGYFGPKCYMILFYPERNT	PAYFNSMIQYTM	RDRD 839

RESULT 5

US-10-725-489-6
; Sequence 6, Application US/10725489
; Publication No. US20040175793A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,489
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21

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; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-725-489-6

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	Query Match	100.0%;	Score 4443;	DB 16;	Length 839;		
	Best Local Similarity	100.0%;	Pred. No. 0;				
	Matches 839;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	MGPRAKTICSLFFLLVWLAEP	AEANSDFYLP	GDYLLGGLFSLHANMKGIVHLN	FLQVPMCK 60		
Dd	1	MGPRAKTICSLFFLLVWLAEP	AEANSDFYLP	GDYLLGGLFSLHANMKGIVHLN	FLQVPMCK 60		
Qy	61	EYEVKVIGYNLMQAMRFAVEE	INNDSLLPGV	LLGYEIVDV	VCYISNNVQPVLYFLAHEDN 120		
Dd	61	EYEVKVIGYNLMQAMRFAVEE	INNDSLLPGV	LLGYEIVDV	VCYISNNVQPVLYFLAHEDN 120		
Qy	121	LLPIQEDYSNYISRVAVIGPD	NSESVMTVANF	LSLFLLPQIT	YSAISDEL	RDKVRFPAL 180	
Dd	121	LLPIQEDYSNYISRVAVIGPD	NSESVMTVANF	LSLFLLPQIT	YSAISDEL	RDKVRFPAL 180	
Qy	181	LRTTPSADHHVEAMVQMLM	LHFRWNII	VLVSSDTYGRD	NGQLLGERVARRD	ICIAFOETL 240	
Dd	181	LRTTPSADHHVEAMVQMLM	LHFRWNII	VLVSSDTYGRD	NGQLLGERVARRD	ICIAFOETL 240	
Qy	241	PTLQPNQNTSEBRQLVTI	VDKLQOSTAR	VVVVFS	PDLTLYHFFNEVLRQ	NFTGAVWIA 300	
Dd	241	PTLQPNQNTSEBRQLVTI	VDKLQOSTAR	VVVVFS	PDLTLYHFFNEVLRQ	NFTGAVWIA 300	
Qy	301	SESWAIDPVLHNLTELGH	LGTFLGITIQSV	PIPGSEFREWGP	QAGPPPLS	RTSQSYTCN 360	
Dd	301	SESWAIDPVLHNLTELGH	LGTFLGITIQSV	PIPGSEFREWGP	QAGPPPLS	RTSQSYTCN 360	
Qy	361	QECDNCLNATLSFNTIL	RLSGERVVYS	AVYAVAHALH	SLGLGCDKSTCT	KRVVYPWOL 420	
Dd	361	QECDNCLNATLSFNTIL	RLSGERVVYS	AVYAVAHALH	SLGLGCDKSTCT	KRVVYPWOL 420	
Qy	421	LEEIWKVNFLLDHO	IFDPQGDVALH	LEIVQWQDR	SQNPFOQSV	ASYYPQLRQLNQID 480	
Dd	421	LEEIWKVNFLLDHO	IFDPQGDVALH	LEIVQWQDR	SQNPFOQSV	ASYYPQLRQLNQID 480	
Qy	481	ISWHTVNNTIPMSMCS	KRCQSGQKKP	VGIVHCCFEC	IDCLPGTFLN	HTEDEYECQACP	N 540
Dd	481	ISWHTVNNTIPMSMCS	KRCQSGQKKP	VGIVHCCFEC	IDCLPGTFLN	HTEDEYECQACP	N 540
Qy	541	NEWSYQSETSCFKRQL	VLEWHEAPTIA	VALLAALGFL	STLAILVIFWR	HFQTPIVRSAG 600	
Dd	541	NEWSYQSETSCFKRQL	VLEWHEAPTIA	VALLAALGFL	STLAILVIFWR	HFQTPIVRSAG 600	
Qy	601	GPMCFLMTLLLVAYMV	VPVVVGGPKV	STCLCRQAL	FPLCFTICIS	CIASVRSFQIVCAFK 660	
Dd	601	GPMCFLMTLLLVAYMV	VPVVVGGPKV	STCLCRQAL	FPLCFTICIS	CIASVRSFQIVCAFK 660	
Qy	661	MASRFPRAYSYWRV	YQGPYVSM	AFITVLKM	VIVIGMLAT	GLSPTRTDPDP	DKITIVSC 720
Dd	661	MASRFPRAYSYWRV	YQGPYVSM	AFITVLKM	VIVIGMLAT	GLSPTRTDPDP	DKITIVSC 720
Qy	721	NPNYRNSLLENTSL	DLLSVVGFS	FAYMGKELPT	NYNEAKFIT	LSMTFYFTSS	VSLSCTFM 780
Dd	721	NPNYRNSLLENTSL	DLLSVVGFS	FAYMGKELPT	NYNEAKFIT	LSMTFYFTSS	VSLSCTFM 780
Qy	781	SAYSGVLVTIVD	LLVTVLNLLAIS	LGYPGPKCYM	ILFYPER	NTPAYFN	SMIQYTMRRD 839
Dd	781	SAYSGVLVTIVD	LLVTVLNLLAIS	LGYPGPKCYM	ILFYPER	NTPAYFN	SMIQYTMRRD 839

		Best Local Similarity 100.0%; Pred. No. 0;																						
		Matches	Conservative	0;	Mismatches																			
		0;	Indels	0;	Gaps																			
		0;																						
QY	1	MGPRAKTICSLFFLLWVLA	BP	AE	NS	DF	YLP	PG	DY	LL	GG	LS	HL	HA	MM	KG	IV	HL	NF	LO	VP	MC	60	
Db	1	MGPRAKTICSLFFLLWVLA	BP	AE	NS	DF	YLP	PG	DY	LL	GG	LS	HL	HA	MM	KG	IV	HL	NF	LO	VP	MC	60	
QY	61	EYEVKVI	GY	NL	MQ	AM	RF	AE	EE	IN	ND	SS	LL	PG	V	LL	GY	E	I	VD	V	CY	IS	120
Db	61	EYEVKVI	GY	NL	MQ	AM	RF	AE	EE	IN	ND	SS	LL	PG	V	LL	GY	E	I	VD	V	CY	IS	120
QY	121	LLPIQEDYS	NY	IS	RV	VA	IG	PD	NS	ES	VM	T	VA	NF	LS	FL	L	P	Q	I	T	Y	SA	180
Db	121	LLPIQEDYS	NY	IS	RV	VA	IG	PD	NS	ES	VM	T	VA	NF	LS	FL	L	P	Q	I	T	Y	SA	180
QY	181	LRTTPSAD	HH	VE	AM	V	Q	L	M	L	H	F	R	W	N	I	I	V	L	V	S	D	T	240
Db	181	LRTTPSAD	HH	VE	AM	V	Q	L	M	L	H	F	R	W	N	I	I	V	L	V	S	D	T	240
QY	241	PTLQPNQ	N	M	T	S	E	R	Q	L	V	T	I	V	D	K	L	Q	S	T	A	R	V	300
Db	241	PTLQPNQ	N	M	T	S	E	R	Q	L	V	T	I	V	D	K	L	Q	S	T	A	R	V	300
QY	301	SES	W	A	I	D	P	V	L	N	L	T	E	L	G	L	T	G	I	T	I	Q	S	360
Db	301	SES	W	A	I	D	P	V	L	N	L	T	E	L	G	L	T	G	I	T	I	Q	S	360
QY	361	QEC	N	C	L	N	A	T	L	S	F	N	T	I	L	S	G	E	R	V	V	S	A	420
Db	361	QEC	N	C	L	N	A	T	L	S	F	N	T	I	L	S	G	E	R	V	V	S	A	420
QY	421	LEE	I	W	K	V	N	F	T	L	D	H	Q	I	F	F	D	P	Q	D	V	A	L	480
Db	421	LEE	I	W	K	V	N	F	T	L	D	H	Q	I	F	F	D	P	Q	D	V	A	L	480
QY	481	I	S	W	H	T	V	N	T	I	P	M	S	M	C	S	K	R	C	S	Q	K	K	540
Db	481	I	S	W	H	T	V	N	T	I	P	M	S	M	C	S	K	R	C	S	Q	K	K	540
QY	541	N	E	S	Y	Q	S	E	T	S	C	F	K	R	Q	L	V	F	L	E	W	H	E	600
Db	541	N	E	S	Y	Q	S	E	T	S	C	F	K	R	Q	L	V	F	L	E	W	H	E	600
QY	601	G	P	M	C	F	L	M	L	T	L	L	V	A	M	V	P	V	Y	G	P	P	K	660
Db	601	G	P	M	C	F	L	M	L	T	L	L	V	A	M	V	P	V	Y	G	P	P	K	660
QY	661	M	A	S	R	F	P	R	A	S	Y	W	R	Y										

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; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-276-21

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RESULT 9
US-10-770-127-198
; Sequence 198, Application US/10770127
; Publication No. US20040214239A1
; GENERAL INFORMATION:
; APPLICANT: SERVANT, GUY
; APPLICANT: OZECK, MARK
; APPLICANT: BRUST, PAUL
; APPLICANT: XU, HONG
; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS
; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R
; TITLE OF INVENTION: AND T2R MODULATORS
; FILE REFERENCE: 100337.54281US
; CURRENT APPLICATION NUMBER: US/10/770,127
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/444,172
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/457,318
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-127-198

Query Match      100.0%; Score 4443; DB 17; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGLGSLHANMKGIVHNLFLQVPMCK 60
Db 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGLGSLHANMKGIVHNLFLQVPMCK 60

QY 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120

QY 121 LLPIQEDYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVFPAL 180
Db 121 LLPIQEDYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVFPAL 180

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICI AFOETL 240
Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICI AFOETL 240

QY 241 PTLOPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFEFNEVL RQNFTGAVWIA 300
Db 241 PTLOPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFEFNEVL RQNFTGAVWIA 300

QY 301 SESWAIDPVLHNLTELGHGTFLGITI IQSVPIPGFSEFREWGPQAGPPPLSRTS QSYTCN 360
Db 301 SESWAIDPVLHNLTELGHGTFLGITI IQSVPIPGFSEFREWGPQAGPPPLSRTS QSYTCN 360

QY 361 QECNCLNATLSFNTILRLSGERVVYSVAVYAVAHALSHLLGCDKSTCTKRVVY PWOQL 420
Db 361 QECNCLNATLSFNTILRLSGERVVYSVAVYAVAHALSHLLGCDKSTCTKRVVY PWOQL 420

QY 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYPLQ RQLKNIQD 480
Db 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYPLQ RQLKNIQD 480

QY 481 ISWHTVNNTIPMSCKSRQSGQKKKPVGIHVCCFECIDCLPGTFLNHTED EYECQACPN 540
Db 481 ISWHTVNNTIPMSCKSRQSGQKKKPVGIHVCCFECIDCLPGTFLNHTED EYECQACPN 540

QY 541 NEWSYQSETSCFRQLVFLWEHAPTIAVALLAALGFLSTLAILVIFWRHFQ TPVRSAG 600
Db 541 NEWSYQSETSCFRQLVFLWEHAPTIAVALLAALGFLSTLAILVIFWRHFQ TPVRSAG 600

QY 601 GPMCFMLTLLLVAYMVVPVYVGPVKVSTCLCRQALFPLCFTICISCI AVRSFQIVCAFK 660
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Db 601 GPMCFMLTLLLVAYMVVPVYVGPVKVSTCLCRQALFPLCFTICISCI AVRSFQIVCAFK 660
QY 661 MASRFPFRAYSWVRYQGPVSMAFITVLKQVIVVIGMLATGLSPTRTDDPDPK ITIVSC 720
Db 661 MASRFPFRAYSWVRYQGPVSMAFITVLKQVIVVIGMLATGLSPTRTDDPDPK ITIVSC 720
QY 721 NPNYRNSLLPNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
Db 721 NPNYRNSLLPNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839
Db 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNMSIQGYTMRD 839

RESULT 10
US-10-246-785-4
; Sequence 4, Application US/10246785
; Publication No. US20030148448A1
; GENERAL INFORMATION:
; APPLICANT: IRM, LLC
; APPLICANT: The Scripps Research Institute
; APPLICANT: Liao, Jiayu
; APPLICANT: Sheng, Ding
; APPLICANT: Schultz, Peter G
; TITLE OF INVENTION: Sweet Taste Receptors
; FILE REFERENCE: 36-002810US/PC
; CURRENT APPLICATION NUMBER: US/10/246,785
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/323,450
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-785-4
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Query Match      99.5%; Score 4422; DB 14; Length 839;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 834; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGLGSLHANMKGIVHNLFLQVPMCK 60
Db 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGLGSLHANMKGIVHNLFLQVPMCK 60

QY 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db 61 EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120

QY 121 LLPIQEDYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVFPAL 180
Db 121 LLPIQEDYSNYSIRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVFPAL 180

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICI AFOETL 240
Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDTYGRDNGQLLGERVARRDICI AFOETL 240

QY 241 PTLOPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFEFNEVL RQNFTGAVWIA 300
Db 241 PTLOPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFEFNEVL RQNFTGAVWIA 300

QY 301 SESWAIDPVLHNLTELGHGTFLGITI IQSVPIPGFSEFREWGPQAGPPPLSRTS QSYTCN 360
Db 301 SESWAIDPVLHNLTELGHGTFLGITI IQSVPIPGFSEFREWGPQAGPPPLSRTS QSYTCN 360

QY 361 QECNCLNATLSFNTILRLSGERVVYSVAVYAVAHALSHLLGCDKSTCTKRVVY PWOQL 420
Db 361 QECNCLNATLSFNTILRLSGERVVYSVAVYAVAHALSHLLGCDKSTCTKRVVY PWOQL 420

QY 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYPLQ RQLKNIQD 480
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Db 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYYPQLQKNIQD 480
QY 481 ISWHTVNNTIPMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTINNTPMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMLTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
Db 601 GPMCFLMLTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
QY 661 MASRFPRAYSYWRVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPDPKITIVSC 720
Db 661 MASRFPRAYSYWRVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPDPKITIVSC 720
QY 721 NPNYRNSLLENTSLDILLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
Db 721 NPNYRNSLLENTSLDILLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 839
Db 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 839

RESULT 11

US-09-927-315-9
; Sequence 9, Application US/09927315
; Publication No. US20030040045A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/09/927,315
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T1R2 sweet taste receptor
US-09-927-315-9

Query Match 98.9%; Score 4392.5; DB 10; Length 838;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 MGPRAKTICSLFFLLVLAEPAEANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
Db 1 MGPRAKTICSLFFLLVLAEPAEANSDFYLPDGYLLGGLFSLHANMKGIVHLNFIQVPMCK 60
QY 61 EYEVKVIQYNLMQAMREAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db 61 EYEVKVIQYNLMQAMREAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
QY 121 LLIPIQEDYSNYSRVAIVGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL 180

Db 121 LLIPIQEDYSNYSRVAIVGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL 180
QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLLGERVARRDICIQAFQETL 240
Db 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLSSDYGRDNGQLLGERVARRDICIQAFQETL 240
QY 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFFNEVLNQFTGAWWIA 300
Db 241 PTLQPNQNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLYHFFNEVLNQFTGAWWIA 300
QY 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db 301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
QY 361 QECDNCLNATLSFNTILRLSGERVVYSVYAVAHALHSLGCDKSTCTKRVVYPWQL 420
Db 361 QECDNCLNATLSFNTILRLSGERVVYSVYAVAHALHSLGCDKSTCTKRVVYPWQL 420
QY 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYYPQLQKNIQD 480
Db 421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYYPQLQKNIQD 480
QY 481 ISWHTVNNTIPMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
Db 481 ISWHTVNNTIPMSCKRCQSGQKKPVGIHVCCFECIDCLPGTFLNHTDEYECQACPN 540
QY 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db 541 NEWSYQSETSCFKRQLVFLWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
QY 601 GPMCFLMLTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
Db 601 GPMCFLMLTLLLVAYMVVVPVYVGGPKVSTCLCRQALFPLCFTICISCIASVRSFQIVCAFK 660
QY 661 MASRFPRAYSYWRVYQGPVYSMAFITVLKMWIVVIGMLATGLSPTTRTDPDPKITIVSC 720
Db 661 MASRFPRAYSYWRVYQGPVYSMAFITVLKMWIVVIGMLARPOS -HPRTDPPDKITIVSC 719
QY 721 NPNYRNSLLENTSLDILLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 780
Db 720 NPNYRNSLLENTSLDILLSVVGFSEFAYMGKELPTNYNEAKFITLSMTFFYFTSSVSLCTFM 779
QY 781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 839
Db 780 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 838

RESULT 12

US-10-190-417-9
; Sequence 9, Application US/10190417
; Publication No. US20030166137A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Hoon, Mark A.
; APPLICANT: Nelson, Greg
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 02307E-120130US
; CURRENT APPLICATION NUMBER: US/10/190,417
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/358,925
; PRIOR FILING DATE: 2002-02-22

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T1P2
US-10-190-417-9

Query Match 98.9%; Score 4392.5; DB 14; Length 838;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGGFLSLHANMKGIVHLNQLQVPMCK 60
Db |||||
QY 1 MGPRAKTICSLFLLWVLAEPANSDFYLPDYLGGFLSLHANMKGIVHLNQLQVPMCK 60
Db |||||

QY 61 EYEVKVIQYNLMQAMRPAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db |||||
QY 61 EYEVKVIQYNLMQAMRPAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
Db |||||

QY 121 LLPIQEDYSNYSIRVVAVIGPDNSESMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db |||||
QY 121 LLPIQEDYSNYSIRVVAVIGPDNSESMTVANFLSLFLLPQITYSAISDELDRKVRFPAL 180
Db |||||

QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDYGQDNGQLLGERVARRDICIAFOETL 240
Db |||||
QY 181 LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDYGQDNGQLLGERVARRDICIAFOETL 240
Db |||||

QY 241 PTLQPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLHYHFFNEVLNQFTGAVWIA 300
Db |||||
QY 241 PTLQPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTLHYHFFNEVLNQFTGAVWIA 300
Db |||||

QY 301 SESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db |||||
QY 301 SESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
Db |||||

QY 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVVYPWQL 420
Db |||||
QY 361 QECDNCLNATLSFNTILRLSGERVVSVYSAVAVAHALSHLLGCDKSTCTKRVVYPWQL 420
Db |||||

QY 421 LEEIKVNFLLDHIQFFDPQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLKNIQD 480
Db |||||
QY 421 LEEIKVNFLLDHIQFFDPQGDVALHLEIVQWQDRSQNPFSQSVASYPLQRLKNIQD 480
Db |||||

QY 481 ISWHTVNNTPMSMCKRCQSGQKKPVGIHVCCEFCIDCLPGTFLNHTDEYECQACPN 540
Db |||||
QY 481 ISWHTVNNTPMSMCKRCQSGQKKPVGIHVCCEFCIDCLPGTFLNHTDEYECQACPN 540
Db |||||

QY 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db |||||
QY 541 NEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
Db |||||

QY 601 GPMCFMLTLLLVAYMVVPPVGVGPPKVVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660
Db |||||
QY 601 GPMCFMLTLLLVAYMVVPPVGVGPPKVVSTCLCRQALFPLCFTICISCIARSFQIVCAFK 660
Db |||||

QY 661 MASRFPRAYSYWRVYQGPVSMAFITVLKMWIVVIGMLATGLSPTRTDPDDPKITIVSC 720
Db |||||
QY 661 MASRFPRAYSYWRVYQGPVSMAFITVLKMWIVVIGMLARQS-HPRTDPPDDPKITIVSC 719
Db |||||

QY 721 NPNYRNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
Db |||||
QY 720 NPNYRNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 779
Db |||||

QY 781 SAYSGVLVTIVDILLVTNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 839
Db |||||
QY 780 SAYSGVLVTIVDILLVTNLNLAISLGYFGPKCYMILFYPERNTPAYFNSMIQYTMRRD 838
Db |||||

RESULT 13
US-10-124-598-7

; Sequence 7, Application US/10124598
; Publication No. US20020119526A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/10/124,598
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/361,631
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/112,747
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
US-10-124-598-7

Query Match 78.0%; Score 3463.5; DB 13; Length 669;
Best Local Similarity 97.5%; Pred. No. 4.5e-301;
Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY 162 ITYSAISDELDRKVRFPALLRRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDYGQDNGQ 221
Db |||||
QY 1 ITYSAISDELDRKVRFPALLRRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDYGQDNGQ 60
Db |||||

QY 222 LLGERVARRDICIAFOETLPTLQPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTL 281
Db |||||
QY 61 LLGERVARRDICIAFOETLPTLQPNQNMNTSEERQRLVTIVDKLQOSTARVVVVFSPDLTL 120
Db |||||

QY 282 YHFFNEVLNQFTGAVWIASESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGFSEFREW 341
Db |||||
QY 121 YHFFNEVLNQFTGAVWIASESWAIDPVLHNLTELGLHGLTFLGITIQSVPIPGFSEFREW 180
Db |||||

QY 342 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVVSVYSAVAVAHALHS 401
Db |||||
QY 181 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVVSVYSAVAVAHALHS 240
Db |||||

QY 402 LLGCDKSTCTKRVVYPWQLLEEIKVNFLLDHIQFFDPQGDVALHLEIVQWQDRSQNP 461
Db |||||
QY 241 LLGCDKSTCTKRVVYPWQLLEEIKVNFLLDHIQFFDPQGDVALHLEIVQWQDRSQNP 300
Db |||||

QY 462 FQSVASYPLQRLKNIQDISWHTVNNTPMSMCKRCQSGQKKPVGIHVCCEFCIDCL 521
Db |||||
QY 301 FQSVASYPLQRLKNIK-TSLHTVNNTPMSMCKRCQSGQKKPVGIHVCCEFCIDCL 359
Db |||||

QY 522 PGTFNLNHTDEYECQACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTL 581
Db |||||
QY 360 PGTFNLNHTDEYECQACPNNEWSYQSETSCFKRQLVLEWHEAPTIAVALLAALGFLSTL 412
Db |||||

QY 582 AILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAYMVVPPVGVGPPKVVSTCLCRQALFPLCF 641
Db |||||
QY 413 AILVIFWRHFQTPIVRSAGGPMCFMLTLLLVAYMVVPPVGVGPPKVVSTCLCRQALFPLCF 472
Db |||||

QY 642 TICISCIARSFQIVCAFKMASRFPRAYSYWRVYQGPVSMAFITVLKMWIVVIGMLATG 701
Db |||||
QY 473 TICISCIARSFQIVCAFKMASRFPRAYSYWRVYQGPVSMAFITVLKMWIVVIGMLARP 532
Db |||||

QY 702 LSPTRTDPDDPKITIVSCNPNVNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKF 761
Db |||||
QY 533 QS-HPRTDPPDDPKITIVSCNPNVNSLLFNTSLDLLSVVGFSAFYMKGKELPTNYNEAKF 591
Db |||||

QY 762 ITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDILLVTNLNLAISLGYFGPKCYMILFYPER 821
Db |||||

Db 592 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTVLNLLAISLGYFGPKCYMILFYPER 651

QY 822 NTPAYFNSMIQGYTMRRD 839

Db 652 NTPAYFNSMIQGYTMRRD 669

RESULT 14

US-10-096-144-7

; Sequence 7, Application US/10096144

; Publication No. US2003002288A1

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Adler, Jon Elliot

; APPLICANT: Lindemeier, Juergen

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor

; TITLE OF INVENTION: Involved in Sensory Transduction

; FILE REFERENCE: 02307E-088720US

; CURRENT APPLICATION NUMBER: US/10/096,144

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/361,631

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/095,464

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/112,747

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 669

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human G-protein coupled receptor (GPCR) B4 amino

; OTHER INFORMATION: acid sequence

US-10-096-144-7

Query Match 78.0%; Score 3463.5; DB 14; Length 669;

Best Local Similarity 97.5%; Pred. No. 4.5e-301;

Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY 162 ITYSAISDELKDKVRFALLRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQ 221

Db 1 ITYSAISDELKDKVRFALLRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQ 60

QY 222 LLGERVARRDICI AFQETLPTLPQNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTL 281

Db 61 LLGERVARRDICI AFQETLPTLPQNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTL 120

QY 282 YHFFNEVLNQFTGAVWIASWSWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREW 341

Db 121 YHFFNEVLNQFTGAVWIASWSWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREW 180

QY 342 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVWVSVYSAVYAVAHALHS 401

Db 181 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVWVSVYSAVYAVAHALHS 240

QY 402 LLGCDKSTCTKRVVYPWQLLEIWKVNFLLDHQIFFDPQGDVALHLEIVQWQWDRSQNP 461

Db 241 LLGCDKSTCTKRVVYPWQLLEIWKVNFLLDHQIFFDPQGDVALHLEIVQWQWDRSQNP 300

QY 462 FQSVASYYPQLQRLKNIQDISWHTVNTTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 521

Db 301 FQSVASYYPQLQRLKNIK-TSLHTVNTTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 359

QY 522 PGTFLNHTEDEYECQACPNNEWSYQSETSCFKRLVFLWEHAPTIAVALLAALGFLSTL 581

Db 360 PGTFLNHTE-----CPNNEWSYQSETSCFKRLVFLWEHAPTIAVALLAALGFLSTL 412

QY 582 AILVIFWRHFTQPIVRSAGGPMCFMLTLLLVAYMVVVPVVGPPKVSTCLCRQALFPLCF 641

Db 413 AILVIFWRHFTQPIVRSAGGPMCFMLTLLLVAYMVVVPVVGPPKVSTCLCRQALFPLCF 472

QY 642 TICISCI AVRSFOIVCAFKMASRFPRAYSVWVRYQGPYVSMAFITVLKMWIVVIGMLATG 701

Db 473 TICISCI AVRSFOIVCAFKMASRFPRAYSVWVRYQGPYVSMAFITVLKMWIVVIGMLARP 532

QY 702 LSPTRTRDPPDKITIVSCNPNYRNSLLENTSLDILLVWGFSAFYMKGKELPTNYNEAKF 761

Db 533 QS-HPRTRDPPDKITIVSCNPNYRNSLLENTSLDILLVWGFSAFYMKGKELPTNYNEAKF 591

QY 762 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTVLNLLAISLGYFGPKCYMILFYPER 821

Db 592 ITLSMTFYFTSSVSLCTFMSAYSGLVLTIVDILLVTVLNLLAISLGYFGPKCYMILFYPER 651

QY 822 NTPAYFNSMIQGYTMRRD 839

Db 652 NTPAYFNSMIQGYTMRRD 669

RESULT 15

US-10-225-567A-683

; Sequence 683, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 683

; LENGTH: 669

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-683

Query Match 78.0%; Score 3463.5; DB 14; Length 669;

Best Local Similarity 97.5%; Pred. No. 4.5e-301;

Matches 661; Conservative 1; Mismatches 7; Indels 9; Gaps 3;

QY 162 ITYSAISDELKDKVRFALLRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQ 221

Db 1 ITYSAISDELKDKVRFALLRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQ 60

QY 222 LLGERVARRDICI AFQETLPTLPQNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTL 281

Db 61 LLGERVARRDICI AFQETLPTLPQNQNTSEERQRLVTIVDKLQQSTARVVVVFSPDLTL 120

QY 282 YHFFNEVLNQFTGAVWIASWSWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREW 341

Db 121 YHFFNEVLNQFTGAVWIASWSWAIDPVLHNLTELGHGLTFLGITIQSVPIPGFSEFREW 180

QY 342 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVWVSVYSAVYAVAHALHS 401

Db 181 GPQAGPPPLSRTSQSYTCNQCNDCLNATLSFNTILRLSGERVWVSVYSAVYAVAHALHS 240

QY 402 LLGCDKSTCTKRVVYPWQLLEIWKVNFLLDHQIFFDPQGDVALHLEIVQWQWDRSQNP 461

Db 241 LLGCDKSTCTKRVVYPWQLLEIWKVNFLLDHQIFFDPQGDVALHLEIVQWQWDRSQNP 300

QY 462 FQSVASYYPQLQRLKNIQDISWHTVNTTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 521

Db 301 FQSVASYYPQLQRLKNIK-TSLHTVNTTIPMSMCKRCQSGQKKPVGIHVCCFECIDCL 359

QY 522 PGTFLNHTEDEYECQACPNNEWSYQSETSCFKRLVFLWEHAPTIAVALLAALGFLSTL 581

Db 360 PGTFLNHTE-----CPNNEWSYQSETSCFKRLVFLWEHAPTIAVALLAALGFLSTL 412

Qy	582	AILVIFWRHFQTP	IVRSAGGPMCF	MLTL	LLVAYMVVP	VYVGP	PKVSTCLCRQALFPLCF	641
Db	413	AILVIFWRHFQTP	IVRSAGGPMCF	MLTL	LLVAYMVVP	VYVGP	PKVSTCLCRQALFPLCF	472
Qy	642	TICISCI	AVRSFQIVCAFKMASR	FP	RAYSYWVRYQGP	YVSM	AFITVLKMWIVVIGMLATG	701
Db	473	TICISCI	AVRSFQIVCAFKMASR	FP	RAYSYWVRYQGP	YVSM	AFITVLKMWIVVIGMLARP	532
Qy	702	LSPTTR	TD	DDPKITIVSCNP	NYNSLLENTSLD	LLSVVGSFAYMGKELPTNYNEAKF	761	
Db	533	QS-HPRT	DDPKITIVSCNP	NYNSLLENTSLD	LLSVVGSFAYMGKELPTNYNEAKF	591		
Qy	762	ITLSMT	FYFTSSVSLCTFMS	AYSGVLVTIVD	LLVTVLNLLAISLG	YFGPKCYMILFYPER	821	
Db	592	ITLSMT	FYFTSSVSLCTFMS	AYSGVLVTIVD	LLVTVLNLLAISLG	YFGPKCYMILFYPER	651	
Qy	822	NTPAYFNS	MIQGYTMRRD	839				
Db	652	NTPAYFNS	MIQGYTMRRD	669				

Search completed: November 30, 2004, 14:07:27
Job time : 163 secs

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